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OM protein - protein search, using sw model.

Run on: November 15, 2000, 09:46:44 : Search time 17.97 Seconds

(without alignments)  
627.933 Million cell updates/sec

Title: us-08-676-882-2

Perfect score: 1688

Sequence: 1 MAVFEKNTKPKIMVSGMT.....GSIDVEKMKAIALDASK 330

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A. Geneseq 36:\*

- 1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:\*
- 2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:\*
- 3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:\*
- 4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:\*
- 5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT:\*
- 6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:\*
- 7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT:\*
- 8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT:\*
- 9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT:\*
- 10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT:\*
- 11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT:\*
- 12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT:\*
- 13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT:\*
- 14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT:\*
- 15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT:\*
- 16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT:\*
- 17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT:\*
- 18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT:\*
- 19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT:\*
- 20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:\*
- 21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1685	99.8	330	18	W11476
2	828	49.1	315	15	R62605
3	828	49.1	315	20	R01690
4	706	41.8	329	17	R94013
5	421	24.9	319	12	R10591
6	412	24.4	333	10	P91948
7	403	23.9	332	9	P80891
8	398	23.6	316	20	R20054
9	397.5	23.5	314	20	R25997
10	391.5	23.2	328	12	R15736
11	391	23.1	333	18	W33107
12	390	23.1	333	18	W33108

13	371	22.0	295	20	R20055	B. burgdorferi ant
14	356	21.1	381	20	R36058	Extended human sec
15	352.5	20.9	298	11	R08355	Recombinant thermo
16	352.5	20.9	298	11	R09295	Recombinant thermo
17	271	16.1	310	12	R11119	Recombinant L-2-hy
18	240	14.2	374	20	R66184	Human bladder tumo
19	238.5	14.1	338	20	R08576	Mouse MDH protein.
20	229.5	13.6	298	20	R08577	Pig MDH protein.
21	204	12.1	273	18	R29773	Malassezia fungus
22	157.5	9.3	148	20	R29568	Human lung tumour
23	155	9.2	327	14	R34507	T. aquaticus malate
24	148.5	8.8	335	20	R35684	Chlamydia pneumonia
25	143.5	8.5	339	20	R36799	Protein involved in
26	111	6.6	36	20	R01691	Peptide derived from
27	95.5	5.7	395	16	R62956	Chrysanthemyl-diph.
28	95	5.6	308	21	R44811	P. taeda dehydrodi
29	92	5.5	36	20	R01692	Peptide derived from
30	91.5	5.4	470	14	R34471	Hepatitis C virus
31	91	5.4	470	14	R34481	Encoded by Hepatit
32	90.5	5.4	361	18	R26001	Peptidase, Saccha
33	89	5.3	346	20	R37730	Chlamydia trachoma
34	87	5.2	814	16	R11940	gp.trkA fusion use
35	86.5	5.1	361	20	R30738	Amino acid sequenc
36	86.5	5.1	470	14	R34479	Encoded by Hepatit
37	86.5	5.1	470	14	R34480	Encoded by Hepatit
38	86.5	5.1	1014	20	R34478	Porphyromonas ging
39	86.5	5.1	1017	20	R34477	Porphyromonas ging
40	86.5	5.1	1046	20	R34353	Porphyromonas ging
41	85	5.0	450	18	R29454	Streptococcus pneu
42	85	5.0	450	20	R68551	S. pneumoniae Mard
43	84	5.0	207	20	R37432	Chlamydia trachoma
44	84	5.0	490	16	R72566	Penicillium purpur
45	83.5	4.9	3163	16	R94347	Hepatitis GB virus

#### ALIGNMENTS

RESULT	ID	W11476 standard; Protein: 330 AA.
1	W11476	
AC	W11476:	
XX	29-APR-1997 (first entry)	
DE	Elmeria lactate dehydrogenase.	
XX	Lactate dehydrogenase; LDH; coccidiosis; vaccine; vector.	
XX	Elmeria acervulina strain Houghton.	
OS		
XX		
PN	AU9656287-A.	
XX	16-JAN-1997.	
PD		
XX	02-JUL-1996; 96AU-0056287.	
PF		
XX	03-JUL-1995; 95EP-0201801.	
PR		
XX	(ALKU ) AKZO NOBEL NV.	
PA		
XX	Kok JJ, Van Den Boogaart P, Vermeulen AN;	
PI	WPI: 1997-109375/11.	
XX	N-PSDB: T51370.	
DR		
XX	Elmeria lactate dehydrogenase protein - used for prodn. of vaccines	
PT	against coccidiosis in poultry	
XX	Claim 3; Page 20-22; 30pp; English.	
PS		
XX	The 37 kDa lactate dehydrogenase (LDH) (W11476) of Elmeria	
CC		

CC acervulina schizonts, or immunologically active portions of it.  
 CC can be used for prodn. of vaccines against coccidiosis in poultry.  
 CC The LDH can be isolated from schizonts or produced in host cells or  
 CC organisms transformed with recombinant vectors including LDH  
 CC nucleic acids (see also T51370). Live viral vaccines can also be  
 CC produced.  
 CC  
 XX  
 SO Sequence 330 AA;

Query Match 99.8%; Score 1685; DB 18; Length 330;  
 Best Local Similarity 99.7%; Pred. No. 2.5e-160;  
 Matches 329; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVENKTRPKIAMVSGMIGTMAFLCSRLRELDVLPDVPPNMPKAMDISHNSVY 60  
 DB 1 mayfekntrpkiamvsgmigtmaflcsrlreldvlpdvppnmpkamdishnsyv 60  
 QY 61 DPTGTYGSSYECLEKADVYITTAGITKIPGSKDEKSRMDLLPVNIKIMREYGAIRK 120  
 DB 61 dptgtygssyeclekgadvyittagitkpgskdeksrmdllpvnikimreygaiks 120  
 QY 121 YCPNAPVINTNPLDVWVAALQESSGLPHHRICGMAGMLDSSRRPMIADKLEVPDVO 180  
 DB 121 ycpnavintnpldvwvaalqessglphhricgmagmldssrrpmiadklevspdvq 180  
 QY 181 GNVIGVGHDMVPLSRATVNGIPLSEFVKKGMKOEVDIYOKPKVAGEIVRLIGOG 240  
 DB 181 gnvigvghdmvplsratvngiplsefvkkgmkoevdiyokpkvageivrligog 240  
 QY 241 SATYAGASATQMAESTYLKDRKRWVWCSCYLOGGYGVONHYLGVCVIGRGVEKITELE 300  
 DB 241 sayyagasaatqmaestylkdrkrwvwcscylggygvonhylgvcvigrgevetele 300  
 QY 301 LPTQEROELGSDIEVKEMOKATAALDASK 330  
 DB 301 lptqerogelgsdievkemqkataaldask 330

## RESULT 2

R62605 ID R62605 standard; Protein: 315 AA.

AC R62605;

DT 18-JUL-1995 (first entry)

DE P. falciparum lactate dehydrogenase.

KW Lactate dehydrogenase; LDH; immunogen; antibody; immunisation;  
 KM detection; plasma; serum; malaria.

XX Plasmodium falciparum.

PN WO9424287-A.

PD 27-OCT-1994.

PF 06-APR-1994; 94WO-US03796.

PR 12-APR-1993; 93US-0046160.

PA (DART-) DARTMOUTH COLLEGE.

PI Bzik DJ, Fox BA;

DR WPI, 1994-341866/42.

DR N-PSDB; 072947.

PT Isolated gene encoding lactate dehydrogenase of P. falciparum  
 and methods for diagnosis and vaccination against malaria

PS Claim 5; Page 18-19; 35pp; English.

XX  
 CC This sequence represents P. falciparum lactate dehydrogenase (LDH).  
 CC The LDH protein and immunogenic fragments of it may be used as an  
 CC immunogen for antibody generation. The progress of immunisation can  
 CC be monitored by detection of antibody titres in plasma or serum.  
 CC Antibodies raised against fragments of LDH can be used to immunise  
 CC against P. falciparum infection and to detect early malarial  
 CC infection. See also R62606-14.  
 XX  
 SO Sequence 315 AA;

Query Match 49.1%; Score 828; DB 15; Length 315;  
 Best Local Similarity 52.6%; Pred. No. 1.1e-74;  
 Matches 164; Conservative 51; Mismatches 95; Indels 2; Gaps 1;

QY 9 RPKIAMVSGMIGTMAFLCSRLRELDVLPDVPPNMPKAMDISHNSVDTGITVYG 68  
 DB 9 rpkiamvsgmigtmaflcsrlreldvlpdvppnmpkamdishnsvdtgitvsg 68  
 QY 4 kakivlgsgmigtmatlivqknlgvlfdivkmpbhkaldstntvmaynsckvsg 63  
 DB 4 kakivlgsgmigtmatlivqknlgvlfdivkmpbhkaldstntvmaynsckvsg 63  
 QY 69 SNSYECLEKADVYITTAGITKIPGSKDEKSRMDLLPVNIKIMREYGAIRKSYCPNAFVI 128  
 DB 69 snsyeclekgadvyittagitkpgskdeksrmdllpvnikimreygaairksycpnafvi 128  
 QY 64 snlyddlagadvviltagltkpgskdeksrmdllpvlnkimelgshkknopafii 123  
 DB 64 snlyddlagadvviltagltkpgskdeksrmdllpvlnkimelgshkknopafii 123  
 QY 129 NITNPLDVWVAALQESSGLPHHRICGMAGMLDSSRRPMIADKLEVPDVOGMYGVHG 188  
 DB 129 nitnpldvwvaalqessglphhricgmagmldssrrpmiadklevspdvogmygvhg 188  
 QY 189 DHNVPLSRATVNGIPLSEFVKKGMKOEVDIYOKTKVAGEIVRLIGOGSAYAPGA 248  
 DB 189 dhnvplsratvngiplsefvkkgmkoevdiyoktkvageivrligogsayapga 248  
 QY 248 nkmvllkryltvgygiprgefinkklisdealealfdtvtaleivnl--haspyvapa 241  
 DB 248 nkmvllkryltvgygiprgefinkklisdealealfdtvtaleivnl--haspyvapa 241  
 QY 249 SAIQMAESTYLKDRKRWVWCSCYLOGGYGVONHYLGVCVIGRGVEKITELETAOEROE 308  
 DB 249 saiqmaestylkdrkrwvwcscylggygvonhylgvcvigrgeveteleetaoer 308  
 QY 242 ailemaesylkdklkvlicstlllegqyghadifgtpvrvlgangveqleqlinseekak 301  
 DB 242 ailemaesylkdklkvlicstlllegqyghadifgtpvrvlgangveqleqlinseekak 301  
 QY 309 LQGSIDEVKEMO 320  
 DB 309 lqgsidevke 320  
 QY 302 fdealaetkrmk 313  
 DB 302 fdealaetkrmk 313

## RESULT 3

Y01690 ID Y01690 standard; Protein: 315 AA.

AC Y01690;

DT 23-JUN-1999 (first entry)

DE A Plasmodium falciparum lactate dehydrogenase.

KW Lactate dehydrogenase; LDH; antibody; antigenic peptide; malaria;  
 KM immunization; Plasmodium falciparum infection.

XX Plasmodium falciparum.

PN WO9913903-A1.

PD 25-MAR-1999.

PF 08-SEP-1998; 98WO-US18626.

PR 17-SEP-1997; 97US-0932194.

PA (DART-) DARTMOUTH COLLEGE.

PI Bzik DJ, Fox BA;

DR WPI, 1999-229405/19.

DR N-PSDB; X26909.

PT New antibodies to Plasmodium falciparum

PS Claim 1: Page 36-37; 46pp; English.

CC The present sequence represents a Plasmodium falciparum lactate  
CC dehydrogenase (LDH). The specification describes an antibody  
CC which binds to antigenic peptides derived from the LDH  
CC protein. The antibody can be used for diagnosing or treating  
CC malaria in a subject. The peptides and portions can be used  
CC for immunizing an individual against malaria and the antibody  
CC can also be used for diagnosing Plasmodium falciparum infections.

XX Sequence 315 AA;

Query Match 49.1%; Score 828; DB 20; Length 315;  
Best Local Similarity 52.6%; Pred. No. 1.1e-74;  
Matches 164; Conservative 51; Mismatches 95; Indels 2; Gaps 1;

OY 9 RPKIAWGSNGMGTMALFSLRELGDVLEFDVVPNMPKRAMDISHNSVVDGTIVG 68  
DB 4 kaktivvgsgm199vmatlivgknlgdvvlfdlvkmphgkaldstlnvmaysnckvsg 63  
OY 69 SNSYECLGADVITITAGITKIPGSKDEKSRMDLLPVNIKIREVGAIAKSCPNAFVI 128  
DB 64 sntyddlagadvivivagftkapykdekwrrddllplinkimtelgghlkkncpnafil 123  
OY 129 NITNPLDVWVAALQESSGLPHHRICMGAGMLDSSRRFRIADKLEVSPROVGAVIGVHG 188  
DB 124 vvtlnpvdwvqllhghsgvypknkligvldtsrlkkyisqklnvcprdnahvaghg 183  
OY 189 DHNVPLSRATVNGIPLSEFVKKGWIKOEVDIYOKTKVAGETIVRLDGGSAVYAPGA 248  
DB 184 nmwvllkryltvgyrpldgelinkllsdaelafdrvtalaleynl--haaspyvapa 241  
OY 249 SAIQMAESYLADKRKRWVSCYLGQGVQVONHYLGVPCVIGRGVEKIIETELTAOROE 308  
DB 242 altemaesylkdlkkvllscstlllegyshtdltgtpvllgavngveglalqlnseekak 301  
OY 309 LOGSIDEVKEKQ 320  
DB 302 fdaaiaetkrmk 313

RESULT 4

R94013 R94013 standard; Protein; 329 AA.

AC R94013;

DT 21-AUG-1996 (first entry)

DE Heat resistant maleate dehydrogenase.

KW Heat resistant maleate dehydrogenase; h-rMAD; NADH; L-aspartic acid;  
alpha-ketoglutaric acid; glutamine oxalo-transaminase activity; GOT.

OS Bacillus stearothermophilus ATCC 12016.

XX Key Location/Qualifiers

FT Misc-difference 185 /note= "Given in the specification as Var"

PN JP08047389-A.

PD 20-FEB-1996.

PF 01-JUL-1994; 94JP-0151045.

PR 03-JUN-1994; 94JP-0121629.

PR 02-JUL-1993; 93JP-0164701.

PA (TOYO ) TOYOBO KK.

XX WPI; 1996-166248/17.

DR N-PSDB; T17715.

PT Protein having heat resistant maleate dehydrogenase activity - and  
PT reagent cong. protein, NADH and L-aspartic and alpha-keto-glutaric  
acid for determination of glutamine oxalo-transaminase activity

PS Claim 8; Page 13-15; 17pp; Japanese.

CC This sequence represents a protein having heat resistant maleate  
CC dehydrogenase (h-rMAD) activity. The protein has a residual activity  
CC after storage at 40 deg.C for 10 days of at least 60%, pref. 70%  
CC and esp. 90%. A reagent containing the h-rMAD protein, NADH and L-  
CC aspartic and alpha-ketoglutaric acid may be used for the  
CC determination of glutamine oxalo-transaminase (GOT) activity. The h-  
CC rMAD protein may be produced by transforming E. coli with the DNA  
CC encoding this protein and isolating the protein from the culture medium.

XX Sequence 329 AA;

Query Match 41.8%; Score 706; DB 17; Length 329;  
Best Local Similarity 45.3%; Pred. No. 1.9e-62;  
Matches 136; Conservative 64; Mismatches 88; Indels 12; Gaps 3;

OY 9 RPKIAWGSNGMGTMALFSLRELGDVLEFDV--VFNMPKRAMDISHNSVVDGTIVG 66  
DB 5 rkksivvgagftgatafllaqkelgdvvlvdipqlenptkyladmeaspvlgfda 64  
OY 67 YGNSYECLGADVITITAGITKIPGSKDEKSRMDLLPVNIKIREVGAIAKSCPNAF 126  
DB 65 lgsdyadladsdlvltvtagarkpg-----msrdjltvntqklnkvtkevvyspncy 119  
OY 127 VINTNPLDVWVAALQESSGLPHHRICMGAGMLDSSRRFRIADKLEVSPROVGAVIGV 186  
DB 120 lvtlnpvdwvqllhghsgvypknkligvldtsrlkkyisqklnvcprdnahvaghg 179  
OY 187 HGDHNPVLSRATVNGIPLSEFVKKGWIKOEVDIYOKTKVAGETIVRLDGGSAVYAP 246  
DB 180 hgdhnpvlsrvtvgyrpldgelinkllsdaelafdrvtalaleynl--haaspyvapa 234  
OY 247 GASAIQMAESYLADKRKRWVSCYLGQGVQVONHYLGVPCVIGRGVEKIIETELTAOR 306  
DB 235 aasivemveallkdqrrllpalaylegeygyglvlyprrllgngltxkyleleleeteek 294

RESULT 5

R10591 R10591 standard; Protein; 319 AA.

AC R10591;

DT 20-MAR-1991 (first entry)

DE L-lactic acid dehydrogenase.

KW LDH; L-lactic acid; thermophile.

OS Bacillus strain TP-262.

PN JP02286077-A.

PD 26-NOV-1990.

PF 27-APR-1989; 89JP-0108432.

PR 27-APR-1989; 89JP-0108432.

PA (TOYO ) TOYAMA CHEM KK.

XX WPI; 1991-012213/02.

DR O-PSDB; Q10162.

XX Bacillus sp. pref. TP-262 strain - is thermophilic bacterium





PN JP11206385-A.  
 XX  
 PD 03-AUG-1999.  
 XX  
 PF 28-JAN-1998; 98JP-0030594.  
 XX  
 PR 28-JAN-1998; 98JP-0030594.  
 XX  
 PA (MITU ) MITSUBISHI CHEM CORP.  
 XX  
 DR WPI: 1999-486360/41.  
 XX  
 DR N-PSDB; Z09139.  
 PT New lactate dehydrogenase gene and strain destroying gene - useful  
 PT for formation of lactic acid  
 PS Claim 1: Page 11-12; 13pp; Japanese.  
 XX  
 XX This invention describes the isolation of a novel lactate dehydrogenase  
 CC protein from *Brevibacterium flavum* strain Mj-233. The invention also  
 CC describes a microbial strain destroying the lactate dehydrogenase gene of  
 CC a microbe in which the lactate dehydrogenase gene is destroyed by a  
 CC homologous recombination of the above DNA or the above recombinant vector  
 CC DNA with the lactate dehydrogenase gene on the chromosome DNA of the  
 CC microbe cell and a method for the preparation of an amino acid or an  
 CC dehydrogenase gene in which the above strain destroying the lactate  
 CC organic acid (except lactic acid) is collected from the culture.  
 CC Formation of lactic acid in the preparation of an amino acid and an  
 CC organic acid can be decreased with no control of oxygen concentration  
 CC during culture. This sequence represents the lactate dehydrogenase  
 CC protein described in the specification.  
 XX  
 SQ Sequence 314 AA:

Query Match 23.5%; Score 397.5; DB 20; Length 314;  
 Best Local Similarity 29.7%; Pred. No. 1.2e-31;  
 Matches 93; Conservative 76; Mismatches 133; Indels 11; Gaps 6;  
 QY 11 KIAMGSGMIGTMAFLCSIRELGD-VLFEDVVPNMPGRAMDISHNSVVDGTGYGS 69  
 DB 8 KAVLIGAGVGVYAYALLNGMADHAIIDIDDKLEGVMMDINHGVVADERTRVTKG 67  
 QY 70 NSEELCKAGDVVITTAGITRKIPKSKDKEMRMDLLPVNRIKIMRE-VGAIKSYCPNAEVI 128  
 DB 68 LYADC-EDAMVVICAGAAQKPGE-----RLQLVKNVKIMKSIYGVMAISGFDGIFLV 121  
 QY 129 NITNPLDVVAALQESSGLPHHRICGMAGMLDSSRRFRMIADKLEVSPPROQGVICVHG 188  
 DB 122 -ASNPVDILTYAVKTSGLIEMNVI9SGTVIDSARITRMIGELYEVAAPSSHAYIIGEHG 180  
 QY 189 DHMVLISRYATVNGIPLSEFVKKGMIKOEVEDIVOKTKVAGEIYVLLQGSAYAFPGA 248  
 DB 181 dtelpylsatlaagvslsmldkpelegrlekifedtrdaayhld--akgstsyigim 238  
 QY 249 SAIDMAESTLYKDRKRWKSCYLOGOYGVONHLYGVCVIGGKVEKIIELELTAEOROE 308  
 DB 239 gjarltraylqngdvaavpysallhgeygeediyigpavvnrrigtrivveltdhemer 298  
 QY 309 LOGSIDEVKEKOK 321  
 DB 299 fksantltreiq 311

RESULT 10  
 ID R15736 standard; Protein: 328 AA.  
 XX R15736;  
 AC R15736;  
 DE 17-MAR-1992 (first entry)  
 DT  
 XX

DE L-lactic acid dehydrogenase.  
 XX  
 XX Recombinant.  
 KM  
 XX  
 OS Streptococcus thermophilus.  
 XX  
 XX JP03251172-A.  
 PN  
 XX  
 PD 08-NOV-1991.  
 XX  
 PF 28-FEB-1990; 90JP-0045967.  
 XX  
 PR 28-FEB-1990; 90JP-0045967.  
 XX  
 PA (MEIJ ) MEIJI MILK PRODS KK.  
 XX  
 DR WPI: 1991-373410/51.  
 DR N-PSDB; Q15280.  
 XX  
 XX New L-lactic acid dehydrogenase and gene encoding it - for  
 PT producing L-lactic acid in vitro in high yield from pyruvic acid  
 PT  
 PS Claim 1: Fig 1: 9pp; Japanese.  
 XX  
 XX The sequence is that of a new L-lactic acid dehydrogenase which may  
 CC produced in large amts. The enzyme can produce lactic acid in vitro  
 CC from pyruvic acid and may be produced directly by culturing a  
 CC transformed bacteria in which the gene is introduced.  
 XX  
 SQ Sequence 328 AA:

Query Match 23.2%; Score 391.5; DB 12; Length 328;  
 Best Local Similarity 29.2%; Pred. No. 5.2e-31;  
 Matches 92; Conservative 75; Mismatches 127; Indels 21; Gaps 7;  
 QY 11 KIAMGSGMIGTMAFLC-----SIRELGDVLFEDVVPNM---PMGRAMDISHNSVVDGTG 63  
 DB 9 KAVLIGAGVGVYAYALLNGMADHAIIDIDDKLEGVMMDINHGVVADERTRVTKG 62  
 QY 64 ITVYGSNSYCLKAGADVITTAGITRKIPKSKDKEMRMDLLPVNRIKIMREYGAIAIKSYCP 123  
 DB 63 PKLIAKACDADADLVLTAGAPKPGE-----RLDIVGKHLANKSIVGVESGF 117  
 QY 124 NAEVINITNPLDVVAALQESSGLPHHRICGMAGMLDSSRRFRMIADKLEVSPPROQGVICVHG 183  
 DB 118 NGFLVVAOPVDILTYAVKTSGLIEMNVI9SGTVIDSARITRMIGELYEVAAPSSHAYIIGEHG 177  
 QY 184 IGVGDMHVLISRYATVNGIPLSEFVK-KGMIKOEVEDIVOKTKVAGEIYVLLQGSAYAFPGA 242  
 DB 178 MGEHGDSEFAVSHANLAGVNLAEFLKDKENYGEAEIVELFEYVIDAYTLIN--KKGAT 235  
 QY 243 YVAPGASAIOMAESYKDRKRWKSCYLOGOYGVONHLYGVCVIGGKVEKIIELELTAEOROE 302  
 DB 236 YGSLAVALARITKALIDDENAVIPLSVFGEGYGVNMLIFGPAIYGAHJIVPVNPLN 295  
 QY 303 AOEROELGOSIDEVK 317  
 DB 296 daeqkmkasadelq 310

RESULT 11  
 ID W33107 standard; Protein: 333 AA.  
 XX W33107;  
 AC W33107;  
 DE 28-JAN-1998 (first entry)  
 DT  
 XX  
 XX Chicken lactic acid dehydrogenase type B subunit.  
 XX  
 KM Chicken: lactic acid dehydrogenase; LDH; type B subunit; tetramer;  
 KM CUDH-B4 isozyme; reagent; transaminase; determination.

XX Gallus domesticus.  
 OS JP09262089-A.  
 XX  
 XX  
 XX 07-OCT-1997.  
 PD  
 XX  
 XX 28-MAR-1996; 96JP-0073797.  
 PF  
 XX 28-MAR-1996; 96JP-0073797.  
 PR  
 XX (ORIV ) ORIENTAL YEAST CO LTD.  
 XX  
 XX WPI: 1997-544152/50.  
 DR N-PSDB; T88365.  
 XX  
 XX DNA encoding chicken lactic acid dehydrogenase type B subunit -  
 PT which can form tetramer, useful as reagent for transaminase activity  
 PT determination  
 XX  
 XX Claim 1; Pages 9-10; 16pp; Japanese.  
 PS  
 XX  
 CC The present sequence is chicken lactic acid dehydrogenase  
 CC (LDH) type B subunit, which can form a tetramer to give CLDH-B4  
 CC isozyme. The CLDH-B4 isozyme can be used as a reagent for  
 CC transaminase activity determination.  
 XX  
 SQ Sequence 333 AA;

Query Match 23.28; Score 391; DB 18; Length 333;  
 Best Local Similarity 29.98; Pred. No. 6e-31;  
 Matches 97; Conservative 69; Mismatches 138; Indels 20; Gaps 8;

OY 11 KIAWGSIGMGTAFLCSLRELG----DVLFEDVVPNMPGKAMDISHNSVVDGCT 65  
 DB 22 KILVGVGVGVG----macalsilgkglcdelaivdvledkikgemmdlqhsiflqth-k 76  
 OY 66 VVGSNSYECLKGAADVITITAGITKIPGKSDKESRMDLFPVNIKIMREVGAAIKSYCPNA 125  
 DB 77 Ivaadkyavtanskilvvtavagvtrqge-----srlnlvqnnvnefkflipqivkyspnc 131  
 OY 126 FVITNITPLDVMVAALQESSGLPHHRICGMAGMDSSRFRMTADKLEVSPRDVGWYIG 185  
 DB 132 ILLVSNPVDILLYVTKLSGLPRKRVIGSGCNDTARFYIlaerligihptschgwllg 191  
 OY 186 VHGDMHVPISRAVNGIPSEF-VKKGWIKQEVDDIVQKTVAGG-ETVRLLGGSAY 243  
 DB 192 ehgdssvaavsgvnnvavslqdelnpamgtcdksenwkevhkqvvesayevirl--kqyt 249  
 OY 244 YAPGASAIOMAESYLKDRKRVWCSCYLOGGYGVONH-YGVPVCVIGRGVEKTELELT 302  
 DB 250 waiglsvaaelcelmknlyrvhsvstlvkgytgiendvfispcvlasgltsvlnqklk 309  
 OY 303 AQERQELQGSIDEVKEKOKAIAAL 326  
 DB 310 ddevaqlkksadtlwsiqdkldl 333

RESULT 12  
 ID W33108 standard; Protein: 333 AA.  
 XX  
 AC W33108;  
 XX  
 XX 28-JAN-1998 (first entry)  
 DT  
 XX  
 XX Chicken lactic acid dehydrogenase type B subunit.  
 DE  
 XX Chicken lactic acid dehydrogenase; LDH; type B subunit; tetramer;  
 XX CLDH-B4 isozyme; reagent; transaminase; determination.  
 KM  
 XX Gallus domesticus.  
 OS

XX JP09262089-A.  
 XX  
 XX  
 XX 07-OCT-1997.  
 PD  
 XX  
 XX 28-MAR-1996; 96JP-0073797.  
 PF  
 XX 28-MAR-1996; 96JP-0073797.  
 PR  
 XX (ORIV ) ORIENTAL YEAST CO LTD.  
 XX  
 XX WPI: 1997-544152/50.  
 DR  
 XX  
 XX DNA encoding chicken lactic acid dehydrogenase type B subunit -  
 PT which can form tetramer, useful as reagent for transaminase activity  
 PT determination  
 XX  
 XX Claim 1; Pages 10-11; 16pp; Japanese.  
 PS  
 XX  
 CC The present sequence is chicken lactic acid dehydrogenase  
 CC (LDH) type B subunit, which can form a tetramer to give CLDH-B4  
 CC isozyme. The CLDH-B4 isozyme can be used as a reagent for  
 CC transaminase activity determination.  
 XX  
 SQ Sequence 333 AA;

Query Match 23.18; Score 390; DB 18; Length 333;  
 Best Local Similarity 29.68; Pred. No. 7.5e-31;  
 Matches 96; Conservative 70; Mismatches 138; Indels 20; Gaps 8;

OY 11 KIAWGSIGMGTAFLCSLRELG----DVLFEDVVPNMPGKAMDISHNSVVDGCT 65  
 DB 22 KILVGVGVGVG----macalsilgkglcdelaivdvledkikgemmdlqhsiflqth-k 76  
 OY 66 VVGSNSYECLKGAADVITITAGITKIPGKSDKESRMDLFPVNIKIMREVGAAIKSYCPNA 125  
 DB 77 Ivaadkyavtanskilvvtavagvtrqge-----srlnlvqnnvnefkflipqivkyspnc 131  
 OY 126 FVITNITPLDVMVAALQESSGLPHHRICGMAGMDSSRFRMTADKLEVSPRDVGWYIG 185  
 DB 132 ILLVSNPVDILLYVTKLSGLPRKRVIGSGCNDTARFYIlaerligihptschgwllg 191  
 OY 186 VHGDMHVPISRAVNGIPSEF-VKKGWIKQEVDDIVQKTVAGG-ETVRLLGGSAY 243  
 DB 192 ehgdssvaavsgvnnvavslqdelnpamgtcdksenwkevhkqvvesayevirl--kqyt 249  
 OY 244 YAPGASAIOMAESYLKDRKRVWCSCYLOGGYGVONH-YGVPVCVIGRGVEKTELELT 302  
 DB 250 waiglsvaaelcelmknlyrvhsvstlvkgytgiendvfispcvlasgltsvlnqklk 309  
 OY 303 AQERQELQGSIDEVKEKOKAIAAL 326  
 DB 310 ddevaqlkksadtlwsiqdkldl 333

RESULT 13  
 ID Y20055 standard; Protein: 295 AA.  
 XX  
 AC Y20055;  
 XX  
 XX 19-JUL-1999 (first entry)  
 DT  
 XX  
 XX B. burgdorferi antigenic protein, t874.aa.  
 DE  
 XX Antigenic protein; vaccine; Lyme disease; infection; detection.  
 XX Borrelia burgdorferi.  
 OS  
 XX WO9859071-A1.  
 XX  
 PD 30-DEC-1998.

XX 18-JUN-1998; 98WO-US12718.  
XX  
PR 03-SEP-1997; 97US-0057483.  
PR 20-JUN-1997; 97US-0050359.  
PR 22-JUL-1997; 97US-0053344.  
PR 22-JUL-1997; 97US-0053377.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (MED-) MEDIMUNE INC.  
XX  
PI Choi GH, Erwin AL, Hanson MS, Lathigra R;  
XX  
DR WPI: 1999-189980/16.  
DR N-PSDB: X61752.  
XX  
XX New isolated Borrelia burgdorferi nucleic acids - used to develop  
PT products for the diagnosis, prevention and treatment of diseases  
PT caused by Borrelia, particularly Lyme disease  
XX  
PS Claim 12; Page 177; 275pp; English.  
XX  
CC This sequence represents a Borrelia burgdorferi (Bb) protein of the  
CC invention, which is suitable for use in a vaccine. The Bb polypeptides  
CC can be used in vaccines for eliciting protective antibodies to members of  
CC the Borrelia genus, particularly for the use against Lyme disease in  
CC humans and animals. They can be used for preventing or attenuating an  
CC infection caused by a member of the Borrelia genus. The products can also  
CC be used for detection of members of the Borrelia genus.  
XX  
SQ Sequence 295 AA;  
XX  
Query Match 22.0%; Score 371; DB 20; Length 295;  
Best Local Similarity 28.2%; Pred. No. 5e-29;  
Matches 82; Conservative 79; Mismatches 108; Indels 22; Gaps 7;  
XX  
OY 35 DVALFDVPMRPMGKAMDISHNSVDTGTY-VGSMSYECCKGADVITTAITKTRPK 93  
DB 11 elviivnenkakgevmadnhgmflklnvltfg--lykdcanaadlvitlagdqngkpgc 68  
XX  
OY 94 SDEKMSRMDLLPNIKIMREVGAIKSYCPNATVINITNPLDVNVALDOESSGLPHHRIC 153  
DB 69 -----trldvdknskifkfditlnvssgfdgjfivvasnpvdlmtymkyskfrphkvi 123  
XX  
OY 154 GMAGLDSSFRFPMADKLEVSPPDVQGVNIGVGHMPLSRVAT-----VNGIPLSEF 208  
DB 124 gctgtltdsrlyfshfnvntqnhlsyngexhd-----ssfatwdeklamkplsey 178  
XX  
OY 209 VKKGWIKQEVNDIVOKTVAGSEIYRLLGQSAIYAPGSAIOMAESYTKDRKRWVCS 268  
DB 179 laegkiteltdelrhkknvaayevikl--kgatyyalqigiknlynaigdqnvllpis 236  
XX  
OY 269 CYLOGQYGV--VQNHVYLGVPVIGRGVEKIIIELETAQEOEQLGQSIDEVK 317  
DB 237 syingngyggikidlyigapaivekgykevinfkispekldfnsanglk 287  
XX  
RESULT 14  
X36058  
ID Y36058 standard; Protein; 381 AA.  
XX  
AC Y36058;  
XX  
DT 13-SEP-1999 (first entry)  
XX  
DE Extended human secreted protein sequence, SEQ ID NO. 443.  
XX  
KW Secreted protein; human; cytokine; cellular proliferation; cell movement;  
KW cellular differentiation; immune system regulator; anti-inflammatory;  
KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;  
KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;  
KW genetic disease.

XX OS Homo sapiens.  
XX PN W09931236-A2.  
XX PD 24-JUN-1999.  
XX  
XX 17-DEC-1998; 98WO-1B02122.  
XX  
XX 10-AUG-1998; 98US-0096116.  
XX 17-DEC-1997; 97US-0069957.  
XX 09-FEB-1998; 98US-0074121.  
XX 13-APR-1998; 98US-0081563.  
XX  
XX (GEST ) GENSET.  
XX  
XX Bougueleret L, Duclert A, Dumas Milne Edwards J;  
XX  
XX WPI: 1999-385906/32.  
XX DR N-PSDB: X97742.  
XX  
XX  
XX New isolated human secreted proteins  
XX  
PS Claim 9; Page 379-381; 516pp; English.  
XX  
CC This sequence is encoded by an extended human secreted protein coding  
CC sequence of the invention. The secreted proteins can be used in treating  
CC or controlling a variety of human conditions. The secreted proteins may  
CC act as cytokines or may affect cellular proliferation or differentiation  
CC or may act as immune system regulators, haematopoiesis regulators, tissue  
CC growth regulators, regulators of reproductive hormones or cell movement  
CC or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or  
CC tumour inhibition activity. The DNAs can be used in forensic procedures  
CC to identify individuals or in diagnostic procedures to identify  
CC individuals having genetic diseases resulting from abnormal expression of  
CC the genes corresponding to the extended cDNAs. They are also useful for  
CC constructing a high resolution map of the human chromosomes. They can  
CC also be used for gene therapy to control or treat genetic diseases.  
XX  
SQ Sequence 381 AA;  
XX  
Query Match 21.1%; Score 356; DB 20; Length 381;  
Best Local Similarity 28.1%; Pred. No. 2.3e-27;  
Matches 89; Conservative 73; Mismatches 143; Indels 12; Gaps 7;  
XX  
OY 11 KIMVSGSMIGTMAFLCSLREIGD-VLFDVYPMNMGKAMDISHNSVVDGITYGS 69  
DB 71 ksvlgtgsvgmacaizillkylsdelaivldexkligetmdlqhsptfkmp-nlvcs 129  
XX  
OY 70 NSYECLKGAADVITTAITGTRKPKSKDEKSRMDLLPNIKIMREVGAIKSYCPNATVIN 129  
DB 130 kxyfvtanashvllitgagrxkge-----trlnxqrvnvaifkmlssivqspshcklil 184  
XX  
OY 130 ITNPLDVNVALDOESSGLPHHRICGMAGLDSSFRFPMADKLEVSPPDVQGVNIGVGD 189  
DB 185 vspnvldillyvawkltsafrkxrlilgsgcnllixarffllgqklisheeschgvllgghgd 244  
XX  
OY 190 HMVPLSRVATVNGIPLSEFVK--GMVQ--EVVDIVOKTVAGSEIYRLLGQSAIYAPG 247  
DB 245 ssypvwsgvniagrpklndsdigtddpqrknhvhevatayellkmkyts--waig. 302  
XX  
OY 248 ASAIOMAESYTKDRKRWVCSYLOGQYGV--QNHVYLGVPVIGRGVEKIIIELETAQEOE 306  
DB 303 lsvadltesllknlrhrpstitkgyixeevflsipelngentlnlikikilpree 362  
XX  
OY 307 QELOGSIDEVKEMQKAI 323  
DB 363 ahllksaktlweiqnkl 379  
XX  
RESULT 15  
R08355





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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: November 15, 2000, 09:46:44 ; Search time 26.25 Seconds  
(without alignments)  
210.712 Million cell updates/sec

Title: US-08-676-882-2

Perfect score: 1688  
Sequence: 1 MAVFEKTRPKIAMVSGSMT.....GSTDEVKEMOKAIALDASK 330

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/PCITUS.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1688	100.0	330	3	US-08-676-882-2
2	828	49.1	315	4	PCT-US94-03796-2
3	706	41.6	329	1	US-08-270-013B-2
4	706	41.8	329	1	US-08-838-418-2
5	412	24.4	317	1	US-08-748-068-3
6	412	24.4	333	1	US-08-748-068-1
7	391	23.2	333	2	US-08-869-506-2
8	391	23.2	333	3	US-08-128-967-2
9	390	23.1	333	2	US-08-869-506-3
10	390	23.1	333	3	US-09-128-967-3
11	377.5	22.4	327	1	US-07-748-068-2
12	155	9.2	327	1	US-08-211-682-25
13	87	5.2	814	1	US-08-286-305A-3
14	87	5.2	814	2	US-08-441-104A-3
15	87	5.2	814	2	US-08-440-816A-3
16	85	5.0	450	1	US-08-665-435A-2
17	85	5.0	450	2	US-08-843-309-2
18	84.5	5.0	549	3	US-08-886-886-13
19	84.5	5.0	3491	2	US-07-642-734C-2
20	84.5	5.0	3491	3	US-08-439-009A-2
21	84	5.0	551	3	US-08-886-886-15
22	83	4.9	20	4	PCT-US94-03796-8
23	82.5	4.9	391	2	US-08-759-581B-13
24	82.5	4.9	934	1	US-08-215-805A-80
25	81.5	4.8	396	3	US-08-926-253-2
26	81.5	4.8	396	3	US-09-120-074-2
27	81.5	4.8	438	3	US-08-886-886-2
28	81.5	4.8	883	1	US-08-106-433A-2

29	81	4.8	446	2	US-08-934-481-2	Sequence 2, Appli
30	80	4.7	396	2	US-09-061-337-12	Sequence 12, Appl
31	80	4.7	396	2	US-09-122-129-12	Sequence 12, Appl
32	80	4.7	396	3	US-09-340-991-12	Sequence 12, Appl
33	80	4.7	511	3	US-08-931-952-4	Sequence 4, Appli
34	80	4.7	511	3	US-08-272-247-4	Sequence 4, Appli
35	80	4.7	511	3	PCT-US95-08560-4	Sequence 4, Appli
36	79	4.7	418	3	US-08-844-054-2	Sequence 2, Appli
37	79	4.7	453	1	US-08-374-155A-8	Sequence 8, Appli
38	79	4.7	3033	1	US-07-925-695-5	Sequence 8, Appli
39	79	4.7	396	1	US-07-702-771-1	Sequence 5, Appli
40	78.5	4.7	443	2	US-08-935-450-6	Sequence 1, Appli
41	78.5	4.7	1313	2	US-08-244-537-2	Sequence 6, Appli
42	78.5	4.7	422	4	PCT-US91-01360-2	Sequence 2, Appli
43	78	4.6	746	2	US-08-785-431-4	Sequence 2, Appli
44	78	4.6	788	2	US-08-785-431-2	Sequence 2, Appli
45	78	4.6	788	2	US-08-785-431-2	Sequence 2, Appli

#### ALIGNMENTS

```
RESULT 1
US-08-676-882-2
; Sequence 2, Application US/08676882
; Patent No. 6100241
; GENERAL INFORMATION:
; APPLICANT: Kok, Jacobus Johannes
; APPLICANT: van den Boogaart, Paul
; APPLICANT: Vermeulen, Arnoldus Nicolaas
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Akzo No. 6100241el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/676, 882
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gornley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; TELEFAX: (301) 977-0847
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-676-882-2

Query Match 100.0%; Score 1688; DB 3; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.2e-177;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAVFEKTRPKIAMVSGSMGTAFCLSLRELGVVLEPDVVPNNPMKRAMDISNSSVY 60
DB 1 MAVFEKTRPKIAMVSGSMGTAFCLSLRELGVVLEPDVVPNNPMKRAMDISNSSVY 60
OY 61 DTGIVVGSNSECKGADVITITGIRKCKSKKSKSRDLFPVNIKIREVCAATKS 120
|||||
```

Db 61 DTGTVGSGNSYECLKGADVITITAGITKIPGKSDKEMSRMDLLPVNIKIMREVGAAIKS 120  
OY 121 YCPNFAVINTPDLVMAALQESSGLPHHRICGMAGLDSSFRFMIADKLEVSFRDVO 180  
Db 121 YCPNFAVINTPDLVMAALQESSGLPHHRICGMAGLDSSFRFMIADKLEVSFRDVO 180  
OY 181 GNVICVGHDMVPLSRATVNGICPLSEFVKKGMKIOEVEDDITVQTKVAGGELVRLGGG 240  
Db 181 GNVICVGHDMVPLSRATVNGICPLSEFVKKGMKIOEVEDDITVQTKVAGGELVRLGGG 240  
OY 241 SAYAPGASAIQMAESYIKDKRRVAVSCYLOGGYGVONHLYGVPCVIGRGVEKIEELE 300  
Db 241 SAYAPGASAIQMAESYIKDKRRVAVSCYLOGGYGVONHLYGVPCVIGRGVEKIEELE 300  
OY 301 LTAEROELQSGIDSEVKEMOKAIALDLSK 330  
Db 301 LTAEROELQSGIDSEVKEMOKAIALDLSK 330  
RESULT 2  
PCT-US94-03796-2  
Sequence 2, Application PC/TUS9403796  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: GENE ENCODING THE LACTATE DEHYDROGENASE  
TITLE OF INVENTION: ENZYME OF PLASMODIUM FALCIPARUM  
NUMBER OF SEQUENCES: 15  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/03796  
FILING DATE: 06-APR-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/046,160  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: DCI-066CPC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 315 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-03796-2  
Query Match 49.1%; Score 828; DB 4; Length 315;  
Best Local Similarity 52.6%; Pred. No. 5,9e-83;  
Matches 164; Conservative 51; Mismatches 95; Indels 2; Gaps 1;  
OY 9 RPKIAMVSGMIGTMAFLCSLRELGDVLFVDVVPNMPKRAMDISNSSVVDGTVYG 68  
Db 4 KAKIVLVGSMIGVATLLIVOKNLGDVLFVLYKNMPKRALDSTSTNMAVSNCKVSG 63  
OY 69 SNSEYELKAGADVITITAGITKIPGKSDKEMSRMDLLPVNIKIMREVGAAIKSCPNAFVI 128  
Db 64 SNYEDLAGADVITITAGITKIPGKSDKEMSRMDLLPVNIKIMREVGAAIKSCPNAFVI 123  
OY 129 NITNPDLVMAALQESSGLPHHRICGMAGLDSSFRFMIADKLEVSFRDVOGVNIVHG 188  
Db 124 VTNPDVMAALQESSGLPHHRICGMAGLDSSFRFMIADKLEVSFRDVOGVNIVHG 183  
OY 189 DHMPLSRATVNGICPLSEFVKKGMKIOEVEDDITVQTKVAGGELVRLGGGSAIYAPGA 248  
Db 189 DHMPLSRATVNGICPLSEFVKKGMKIOEVEDDITVQTKVAGGELVRLGGGSAIYAPGA 248

Db 184 NKKVLLKRTYVGGIPLQEFINNKLSDALEAIFDRVTNATALEIVNL--HASPYVAPPA 241  
OY 249 SAIQMAESYIKDKRRVAVSCYLOGGYGVONHLYGVPCVIGRGVEKIEELELTAEROEL 308  
Db 242 AITEMAESTLKDKKVLCSTLLEGGYGHSDIFGTPVIVANGVQVIELQNSEKAK 301  
OY 309 LOGSIDSEVEMQ 320  
Db 302 FDEAIAETKRMK 313  
RESULT 3  
US-08-270-013B-2  
Sequence 2, Application US/08270013B  
Patent No. 5686294  
GENERAL INFORMATION:  
APPLICANT: Sogabe et al.  
TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE  
TITLE OF INVENTION: DEHYDROGENASE ACTIVITY  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leydig, Voit & Mayer, Ltd.  
STREET: Two Prudential Plaza, Suite 4900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 61601-6780  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/270,013B  
FILING DATE: 01-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 164701/1993  
FILING DATE: 02-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Robert F.  
REGISTRATION NUMBER: 27555  
REFERENCE/DOCKET NUMBER: 62321  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 616-5600  
TELEFAX: (312) 616-5700  
TELEX: (25)3533  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 329 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-270-013B-2  
Query Match 41.8%; Score 706; DB 1; Length 329;  
Best Local Similarity 45.3%; Pred. No. 1,7e-69;  
Matches 136; Conservative 64; Mismatches 88; Indels 12; Gaps 3;  
OY 9 RPKIAMVSGMIGTMAFLCSLRELGDVLFVDVVPNMPKRAMDISNSSVVDGTVYG 66  
Db 5 RKKISVIGAGFTGATTAFLAOKELGDVLFVDVLPOLNPKRALDLEASPVLGPDANI 64  
OY 67 YGNSYECLKGADVITITAGITKIPGKSDKEMSRMDLLPVNIKIMREVGAAIKSCPNAF 126  
Db 65 IGTSDYADTDSIVITITAGIARKPG-----MSRDLVTTNOKIMQVTEVVKYISPKY 119  
OY 127 VITNPDLVMAALQESSGLPHHRICGMAGLDSSFRFMIADKLEVSFRDVOGVNIVHG 186  
Db 120 IIVLTNPDMATTVTKESGFPKRNRYIGOSGYLDTRAFRTFAEELINISVYKDVTFGLVG 179  
OY 187 HGDHMPVPLSRATVNGICPLSEFVKKGMKIOEVEDDITVQTKVAGGELVRLGGGSAIYAP 246

Db 180 HGDMVPLVRSYAGIPILEKTIIPK-----DRDAIVERTKGGGEIYNLNGNSAYIAP 234  
OY 247 GASAIOMAESEILKRRKRVMSCSYLOGGYQVONHYLGPVCIYGRGVKRIIELELTQER 306  
Db 235 AASLIVENEAALKDORILPAIAVLEGEYEGYIYLGVPITLGGNGIEKVEIELELTQER 294

## RESULT 4

US-08-838-418-2  
Sequence 2, Application US/08838418  
Patent No. 5744342  
GENERAL INFORMATION:  
APPLICANT: Sogabe et al.  
TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE  
TITLE OF INVENTION: DEHYDROGENASE ACTIVITY  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leydig, Volt & Mayer, Ltd.  
STREET: Two Prudential Plaza, Suite 4900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601-6780  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,418  
FILING DATE: 17-MAR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/270,013  
FILING DATE: 01-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 164701/1993  
FILING DATE: 02-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoover, Allen E.  
REGISTRATION NUMBER: 37354  
REFERENCE/DOCKET NUMBER: 78339  
TELEPHONE: (312) 616-5600  
TELEFAX: (312) 616-5700  
TELEX: (25)3533  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 329 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-838-418-2

Query Match 41.8%; Score 706; DB 1; Length 329;  
Best Local Similarity 45.3%; Pred. No. 1,7e-69;  
Matches 136; Conservative 64; Mismatches 88; Indels 12; Gaps 3;

OY 9 RPKIMVSGMIGTMAFLCSLRELGDVVLFDV--VPNNPMGRANDISINSSVDTGIV 66  
Db 5 RKISIVIGAGFGATTAFLAOKELGDVVLVDIPELENTKKAIDMLASVYLGDIANI 64  
OY 67 YGSNSELKAGDVYITAGIKIKIGSKSKESRMDLFPVNIKIMEVGAALKSYCPNAF 126  
Db 65 IGTSDYADTADSDIVVITAGIARKPG-----MSRDLVYTNOKIMQVKEYVKKSPNCY 119  
OY 127 VINTNPLDVVMAALQESSGLPHRRICGAGMLDSSRFPMIADLKVLEVPVQGVICV 186  
Db 120 IIVLINPVDAMITYYFKESGPFKNVYIGOSGLVDTAREFTVAEELINISVKDVTGFLVG 179

OY 187 HDHNPVLSRATVNGIPLSEFVKKMIKOEVDIVQKTVAGGEIYRLIGGSAIYAP 246  
Db 180 HGDMVPLVRSYAGIPILEKTIIPK-----DRDAIVERTKGGGEIYNLNGNSAYIAP 234  
OY 247 GASAIOMAESEILKRRKRVMSCSYLOGGYQVONHYLGPVCIYGRGVKRIIELELTQER 306  
Db 235 AASLIVENEAALKDORILPAIAVLEGEYEGYIYLGVPITLGGNGIEKVEIELELTQER 294

## RESULT 5

US-08-748-068-3  
Sequence 3, Application US/08748068  
Patent No. 5770410  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Chiral Synthesis  
NUMBER OF SEQUENCES: 15  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/748,068  
FILING DATE: 12-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,959  
FILING DATE: 05-OCT-1994  
APPLICATION NUMBER: GB 92 02033.8  
FILING DATE: 30-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 92 04702.6  
FILING DATE: 04-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 93/00204  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 317 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: (15-16)  
OTHER INFORMATION: /note= "numbering discontinuity"  
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NAME/KEY: Modified-site  
LOCATION: (28-29)  
OTHER INFORMATION: /note= "numbering discontinuity"  
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NAME/KEY: Modified-site  
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OTHER INFORMATION: /note= "numbering discontinuity"  
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NAME/KEY: Modified-site  
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OTHER INFORMATION: /note= "numbering discontinuity"  
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NAME/KEY: Modified-site  
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OTHER INFORMATION: /note= "numbering discontinuity"  
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NAME/KEY: Modified-site  
LOCATION: (69-70)  
OTHER INFORMATION: /note= "numbering discontinuity"  
FEATURE:  
NAME/KEY: Modified-site



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? NAME/KEY: Modified-site
? LOCATION: (87~88)
? OTHER INFORMATION: /note- "- numbering discontinuity"
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? LOCATION: (97~98)
? OTHER INFORMATION: /note- "- numbering discontinuity"
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? NAME/KEY: Modified-site
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? LOCATION: (210~211)
? OTHER INFORMATION: /note- "- numbering discontinuity"
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? NAME/KEY: Modified-site
? LOCATION: (245~246)
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? NAME/KEY: Modified-site
? LOCATION: (249~250)
? OTHER INFORMATION: /note- "- numbering discontinuity"
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? NAME/KEY: Modified-site
? LOCATION: (266~267)
? OTHER INFORMATION: /note- "- numbering discontinuity"
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? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: (279~280)
? OTHER INFORMATION: /note- "- numbering discontinuity"
?
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: (302~303)
? OTHER INFORMATION: /note- "- numbering discontinuity"
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? US-08-748-068-1

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Query Match 24.4% Score 412; DB 1; Length 333;
Best Local Similarity 29.9%; Pred. No. 4.2e-37;
Matches 101; Conservative 73; Mismatches 130; Indels 34; Gaps 10;

OY 5 EKNTRP--KIAMVSGMIGTMAFLCSLRELG-----DVLFDDVPPNPMGKAMDISHNS 57
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
14 QETTPNKRITVGVGVG---MACAISILKSLDELALVDLEKLGEMMDLQHS 69

OY 58 SVVDIGITVYGSNTECLGADVITITAGITKIPGSKDEMSRMDLLPVNIKIREVGAA 117
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
70 LFLQRP-KIVANKRDSVTANSKIIVVYTAGVROEGE-----SRNLVQRNVNVEKTIIPQ 123

OY 118 IKSYPNPFVNITNPLDVVAALDESSGLPHHRICGAMGLDSSFRFRIADKLEVSFR 177
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
124 IVKSPNCLIIIVSNPVLITLYTWKLSGLPKHRVIGSGCNLD SARFRLMAEKLCVHPS 183

OY 178 DVQGVAVGCHGMVPLSRVATVNGIPLSEF-----VKKGWIKOEVDVIOKTKVA 229
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
184 SCHGILTEHGGSSAVVMSGVNAGVSLQQLNPEKGTNDSENW---KEVHRKVESAY- 239

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OY 230 GGEIVRLGSGSAYVAPASAIOMAESYLKDRKRVWVSCYLOGGYOVNH-YLGPVCI 288
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
240 --EVIKL--KGYTNMAIGLSVADLIESMLKNSRHPVSTWQNGYGIENEVFLSPCVL 295

OY 289 GGRVEKIELELTPROEOLGSGIDEXKEMOKAIAL 326
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
296 NARGLTSVINOKLADDEVAOLKNSADTLMGIQKDKDL 333

```

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RESULT 7
US-08-869-506-2
? Sequence 2, Application US/08869506
? Patent No. 5827710
? GENERAL INFORMATION:
? APPLICANT: Uchida, Kohji
? APPLICANT: Matsukawa, Hirokazu
? APPLICANT: Matuo, Yushi
? TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
? TITLE OF INVENTION: LACTATE DEHYDROGENASE
? NUMBER OF SEQUENCES: 11
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: NIXON & VANDERHAYE P.C.
? STREET: 1100 No. 5827710th Giebe Rd. 8th floor
? CITY: Arlington
? STATE: VA
? COUNTRY: USA
? ZIP: 22201-4741
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/869,506
? FILING DATE: 05-JUN-1997
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: JP 73797/1996
? FILING DATE: 29-MAR-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Crawford, Arthur R.
? REGISTRATION NUMBER: 25,327
? REFERENCE/DOCKET NUMBER: 159-43
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 703-816-4000
? TELEFAX: 703-816-4000
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 333 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: Protein
? US-08-869-506-2

```

```

Query Match 23.2% Score 391; DB 2; Length 333;
Best Local Similarity 29.9%; Pred. No. 8.7e-35;
Matches 97; Conservative 69; Mismatches 138; Indels 20; Gaps 8;

OY 11 KIAMVSGMIGTMAFLCSLRELG-----DVLFDDVPPNPMGKAMDISHNSVDTGIT 65
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
22 KITVGVGVG---MACAISITIGKGLCOELALVDLEKLGEMMDLQHSIFLQTH-K 76

OY 66 VYGSNTECLGADVITITAGITKIPGSKDEMSRMDLLPVNIKIREVGAAIKSYCPNA 125
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
77 IVADQVAYATANSKIIVVYTAGVROEGE-----SRNLVQRNVNVEKTIIPQIVKTSFPC 131

OY 126 FVINITNPLDVVAALDESSGLPHHRICGAMGLDSSFRFRIADKLEVSFRDVQGVAVG 185
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
132 TLVYVSNPVDILTYTWKLSGLPKHRVIGSGCNLD TARRFRYI MAERLGIHPTSCHMIIG 191

OY 186 VHGDHNVPLSRVATVNGIPLSEF-VKKGWIKOEVDVIOKTKVAGG-BIVRLGGSAY 243

```

Db 192 EHGDSVAWGVNNGVSLQELNPAWGTDKDENNKEVHKOVESAYEYIRL--KGYTN 249  
OY 244 YAPGASAIQMAESYLKDKRVMVSCYLOGQYGVONH-YLGVPCVIGRGVEKIIETELT 302  
Db 250 WAIGLSVAELCETMLKKNLYRVHSVSTLVKCTYGIENDVFLSLPCVLSASGLTSVINQK 309  
OY 303 AOERQLOGSIIDEVKEKOKAIAAL 326  
Db 310 DDEVOLKRSADTLWSTIQDKDL 333

## RESULT 8

US-09-128-967-2  
Sequence 2, Application US/09128967  
Patent No. 6057141  
GENERAL INFORMATION:  
APPLICANT: Uchida, Kohji  
APPLICANT: Matsukawa, Hirokazu  
APPLICANT: Matuo, Yushi  
APPLICANT: Fujita, Tutosi  
TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN  
LACTATE DEHYDROGENASE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYTE P.C.  
STREET: 1100 No. 6057141th Glebe Rd. 8th floor  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22201-4741  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/128,967  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/869,506  
FILING DATE: 05-JUN-1997  
APPLICATION NUMBER: JP 73797/1996  
FILING DATE: 29-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Crawford, Arthur R.  
REGISTRATION NUMBER: 25,327  
REFERENCE/DOCKET NUMBER: 159-43  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4100  
TELEFAX: 703-816-4000  
INFORMATION FOR SEO ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 333 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-128-967-2

Query Match 23.2%; Score 391; DB 3; Length 333;  
Best Local Similarity 29.9%; Pred. No. 8,7e-35;  
Matches 97; Conservative 69; Mismatches 138; Indels 20; Gaps 8.

OY 11 KIAMGSGHIGTMAFLCGLRELG-----DVLVFDVVPMPMPGKAMDISHNSVDVTGIT 65  
Db 22 KITVVGQVGVG---MACAISIILGKGLCDELALVLDLKDRLKLGEMMDLQHGSLFLQTH-K 76  
OY 66 VVGNSYELCKADAVYIITAGITKIPGKSDKESRMDLIPVNIKIREVGAIAIKVSCPNA 125  
Db 77 IYADNDYATNANSKIYVYTAGYRQDEGE-----SRNLVQRNVNVKFIIPQIVKISPMC 131

OY 126 FVINITNPDLVVAALQESSGLPHHRICGMAGLDSRRFRMIADKLEVSPPRVQGVIG 185  
Db 132 TILVSNPVDILTYVWTKLSGLPKHRVYISGCNLDTRFRFYLMAERLGIHPTSCHGWIIG 191  
OY 186 VGHDMWPLSRVNFVNCIPISEF-VKKGWIKQEEVDIVQKTAVAG-ELVRLLGGSAY 243  
Db 192 EHGDSVAWGVNNGVSLQELNPAWGTDKDENNKEVHKOVESAYEYIRL--KGYTN 249  
OY 244 YAPGASAIQMAESYLKDKRVMVSCYLOGQYGVONH-YLGVPCVIGRGVEKIIETELT 302  
Db 250 WAIGLSVAELCETMLKKNLYRVHSVSTLVKCTYGIENDVFLSLPCVLSASGLTSVINQK 309  
OY 303 AOERQLOGSIIDEVKEKOKAIAAL 326  
Db 310 DDEVOLKRSADTLWSTIQDKDL 333

## RESULT 9

US-08-869-506-3  
Sequence 3, Application US/08869506  
Patent No. 5827710  
GENERAL INFORMATION:  
APPLICANT: Uchida, Kohji  
APPLICANT: Matsukawa, Hirokazu  
APPLICANT: Matuo, Yushi  
APPLICANT: Fujita, Tutosi  
TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN  
LACTATE DEHYDROGENASE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYTE P.C.  
STREET: 1100 No. 5827710th Glebe Rd. 8th floor  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22201-4741  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/869,506  
FILING DATE: 05-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 73797/1996  
FILING DATE: 29-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Crawford, Arthur R.  
REGISTRATION NUMBER: 25,327  
REFERENCE/DOCKET NUMBER: 159-43  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4100  
TELEFAX: 703-816-4000  
INFORMATION FOR SEO ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 333 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-869-506-3

Query Match 23.1%; Score 380; DB 2; Length 333;  
Best Local Similarity 29.6%; Pred. No. 1.1e-34;  
Matches 96; Conservative 70; Mismatches 138; Indels 20; Gaps 8;

OY 11 KIAMGSGHIGTMAFLCGLRELG-----DVLVFDVVPMPMPGKAMDISHNSVDVTGIT 65  
Db 22 KITVVGQVGVG---MACAISIILGKGLCDELALVLDLKDRLKLGEMMDLQHGSLFLQTH-K 76



QY 66 VYGSNSYECLGADVITTAGITKIPGSKDEKMSMDLLPVNIKIMREVGAIKISYCNA 125  
Db 77 IVADKDAVAVTANSKIYVAVTAGVROEGE-----SRLNVORNVNFKETIIPOIYKYSFNC 131  
QY 126 FVINITPLDVMAALDOESSGLPHHRIGCMAGMLDSSFRFRIADKLEVSPPDVGMVIG 185  
Db 132 VILVSNPVDILTYVTWMLKSLPKHRVYSGCNDLTARFRLMERLGIHPTSCGWILG 191  
QY 186 VHGDMVPLSRVATVNGIPLSEF-VKKGMIRQOEVDIVQKTYVAGG-EIYRLGOGSAY 243  
Db 192 EHGDSVAVMGCVNAGVSLQOLDPAMGTDKDEKMKKEVHKQVESAVERL--KGYTN 249  
QY 244 YAPGASAIQMAESYLKDRKRVWCSYLOGQYGVNH-YLGVPVIGRGVEKIEILELT 302  
Db 250 WAIGLSVAELCETMLKNIYRHVSSTLVKGTGIENDVFLSPCVLSASGLTSVINOKLK 309  
QY 303 AOEROELGSDIEVKEKOKAIAAL 326  
Db 310 DDEVAOLKKSADTLMSIQDKDL 333

## RESULT 10

US-09-128-967-3  
Sequence 3, Application US/09128967  
Patent No. 6057141  
GENERAL INFORMATION:  
APPLICANT: Uchida, Kohji  
APPLICANT: Matsukawa, Hirokazu  
APPLICANT: Fujita, Tuvosi  
TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYTE P.C.  
STREET: 1100 NO. 6057141th Giebe Rd. 8th floor  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22201-4741  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/128,967  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/869,506  
FILING DATE: 05-JUN-1997  
APPLICATION NUMBER: JP 73797/1996  
FILING DATE: 29-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Crawford, Arthur R.  
REGISTRATION NUMBER: 25,327  
REFERENCE/DOCKET NUMBER: 159-43  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 333 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-128-967-3

Query Match 23.1%; Score 390; DB 3; Length 333;  
Best Local Similarity 29.6%; Pred. No. 1,1e-34;

Matches 96; Conservative 70; Mismatches 138; Indels 20; Gaps 8;  
QY 11 KIAMGSGMIGGTAFNFCLSRELG-----DYLFPEYVNMFMGKAMDISHNSVVDGIT 65  
Db 22 KITVGVGVG-----MACAISILGKGLDELDVLDKDKGEMMDQHSLSFLQTH-K 76  
QY 66 VYGSNSYECLGADVITTAGITKIPGSKDEKMSMDLLPVNIKIMREVGAIKISYCNA 125  
Db 77 IVADKDAVAVTANSKIYVAVTAGVROEGE-----SRLNVORNVNFKETIIPOIYKYSFNC 131  
QY 126 FVINITPLDVMAALDOESSGLPHHRIGCMAGMLDSSFRFRIADKLEVSPPDVGMVIG 185  
Db 132 VILVSNPVDILTYVTWMLKSLPKHRVYSGCNDLTARFRLMERLGIHPTSCGWILG 191  
QY 186 VHGDMVPLSRVATVNGIPLSEF-VKKGMIRQOEVDIVQKTYVAGG-EIYRLGOGSAY 243  
Db 192 EHGDSVAVMGCVNAGVSLQOLDPAMGTDKDEKMKKEVHKQVESAVERL--KGYTN 249  
QY 244 YAPGASAIQMAESYLKDRKRVWCSYLOGQYGVNH-YLGVPVIGRGVEKIEILELT 302  
Db 250 WAIGLSVAELCETMLKNIYRHVSSTLVKGTGIENDVFLSPCVLSASGLTSVINOKLK 309  
QY 303 AOEROELGSDIEVKEKOKAIAAL 326  
Db 310 DDEVAOLKKSADTLMSIQDKDL 333

## RESULT 11

US-08-748-068-2  
Sequence 2, Application US/08748068  
Patent No. 5770410  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Chiral Synthesis  
NUMBER OF SEQUENCES: 15  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/748,068  
FILING DATE: 12-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,959  
FILING DATE: 05-OCT-1994  
APPLICATION NUMBER: GB 92 02033.8  
FILING DATE: 30-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 92 04702.6  
FILING DATE: 04-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 93/00204  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 327 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: (16-17)  
OTHER INFORMATION: /note- "numbering discontinuity"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: (27-28)  
OTHER INFORMATION: /note- "numbering discontinuity"

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Query Match      9.2%  Score 155;  DB 1;  Length 327;
Best Local Similarity 24.3%  Pred. No. 8.3e-09;
Matches 83;  Conservative 59;  Mismatches 145;  Indels 54;  Gaps 17;

QY  11 KIAWG-SGMIGMAFLCSLRE-LGD-----VLFEDVPPNNPM--GRKAMDISHNSVVD 61
::: | : | | : | : | | |

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Db 6 RAAVGAAGCGYSLPRLIAGCMLGKQPVIILOLEIPQAMKLEGVVMELEDCAPBL 65  
 QY 62 TGTIVYSSNSECKGADVITITGTRIKPEKSPKESRMDLPVNIKIMEVGAIAIKSY 121  
 Db 66 AGLEA-TDDRVAEKADADYAL---VGAAPRKAGME--RBDLLVNGKIFPEGGALAEV 119  
 QY 122 C-PNAFVINTNPADV-MVAALQESSGLPHRIGCMAGMLDSSFRRIADKLEVSPPDV 179  
 Db 120 AKADVAVLVGNPANTNALLAYKNAFGLNPNFTAMT-RDHNRAKQALAKKTGTVDRI 178  
 QY 180 QGNVI-GVHGDHNVPLSRVATVNGIPLSEFYKKGIMKOEVDVIVOKTVAGGEIVRLG 238  
 Db 179 RRTVWGNHNSJTMPPDLFHLAEVDSRPALELVDMETKEVFIPTVAOR---GAALIQARG 234  
 QY 239 QGSAIYAPGASAIQMAESYTKDKR-----RVWVSCYLOQGYGVNHVLCVPCYIG 289  
 Db 235 ASSA-----ASANAALAEHIDWALGTPEGDMVSMAPVS---QGEYGIPEGIVYSFVTA 286  
 QY 290 GRCVEKIE-----LELTAORQLOQSIDVEYKEM 319  
 Db 287 KDCATRYVEGLEINERARKMEITA---QELLDEMEQVKAL 324

## RESULT 13

US-08-286-305A-3  
 : Sequence 3, Application US/08286305A  
 : Patent No. 5766863

## GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.  
 APPLICANT: Mark, Melanie R.  
 APPLICANT: Sadick, Michael D.  
 APPLICANT: Shelton, David L.  
 APPLICANT: Wong, Wal Lee Tan  
 TITLE OF INVENTION: KINASE RECEPTOR ACTIVATION ASSAY  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: palin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/286,305A  
 FILING DATE: 05-AUG-1994  
 CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/170558  
 FILING DATE: 20-DEC-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/157563  
 FILING DATE: 23-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lee, Wendy M.

## REGISTRATION NUMBER: 00,000

REFERENCE/DOCKET NUMBER: 854C1P1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1994  
 TELEFAX: 415/952-9881

TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO. 3:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 814 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

US-08-286-305A-3

Query Match 5.2%; Score 87; DB 1; Length 814;  
 Best Local Similarity 20.1%; Pred. No. 1.1;  
 Matches 71; Conservative 36; Mismatches 83; Indels 164; Gaps 17;

QY 20 IGTMAFLCSLRELDVLFDPVNPMPKAMDISHNSVVDGTITVYSGNSYECLEKAD 79  
 Db 1 MGTAA-----RLGAVILFVFI-----VGLHGVNGKAL--AD 31  
 QY 80 VVITAGTRIKPGSKDEKSRMDLPVNIKIMEVGAIAISYCNAFVINTNPADVVA 139  
 Db 32 ASLMAADPNRRRGD-----LPVLDLLEVAAPCPDACCPHG----- 68  
 QY 140 ALOESSGLPHRIGCMAGMLDSSRF-----RRIADKLEVSPPDVGM----- 182  
 Db 69 -----SSGLR-----CTRGALDSLHLHLGAEMLTELYENQOHLQHLT--RDLGLGELR 118  
 QY 183 -----VIGVGHMVP-ISR-----YATVNGIPLSEFYKKG----- 212  
 Db 119 NLTVKSGLRFAVDAPDFHTPRLSLRLMSFNALESLSMKTYQGLQELVILSGNPLHCSC 178  
 QY 213 ----WIKQEEVDIVQTKKVAGG---EIVRLQGSATYAPGASAIQMAESYLDKRRVMV 266  
 Db 179 ALRWLQWEEEGT-----GVPEQKLOCHGQGPLAHMNPASC----- 215  
 QY 267 CSCYLQGYGVNHVLCVP-----CVIGRGVEK-----IIELETA 303  
 Db 216 -----GVPLTKGVPNASVDVGDVLLRCOVESRGLEQMGWILTELOS 260

## RESULT 14

US-08-441-104A-3  
 : Sequence 3, Application US/08441104A  
 : Patent No. 5891650

## GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.  
 APPLICANT: Mark, Melanie R.  
 APPLICANT: Sadick, Michael D.  
 APPLICANT: Shelton, David L.  
 APPLICANT: Wong, Wal Lee Tan  
 TITLE OF INVENTION: KINASE RECEPTOR ACTIVATION ASSAY  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 720 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: palin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/441,104A  
 FILING DATE: 15-MAY-1995  
 CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/286305  
 FILING DATE: 05-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/170558  
 FILING DATE: 20-DEC-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/157563  
 FILING DATE: 23-NOV-1993  
 ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 00,000

REFERENCE/DOCKET NUMBER: 854C1P1C2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1994  
 TELEFAX: 415/952-9881

TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 814 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-441-104A-3

Query Match 5.2%; Score 87; DB 2; Length 814;  
 Best Local Similarity 20.1%; Pred. No. 1.1;  
 Matches 71; Conservative 36; Mismatches 83; Indels 164; Gaps 17;

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QY 20 IGTMAFLCSLRELGDVDFVPMNPMKAMDISHNSSVVDIGITVYGSNSTECLKAD 79
DB 1 MGSTAA-----RLGAVILFVVI-----VGLHVGKRYAL--AD 31
QY 80 VVITAGITRKIPKSDKEMSRMDLFPNIMREVGAIKSYCPNMFVINITPLDVMA 139
DB 32 ASLKMDPNNFRGKD-----LPVLDQLLEVAAPCPDACCPCG----- 68
QY 140 ALOESSGLPHHRICGAGMLDSRF-----RRMIADKLEVSPRDYGM---- 182
DB 69 -----SSGLR-----CTRDGALDSLHLPGAENLTETYENQOHLQHEL--RDLRGLGELR 118
QY 183 -----VIGVHGDHWP--LSR-----YATVNCIPLSEYVKKG----- 212
DB 119 NLTIVKSGLRFPAPDAFHPTPLRLSLNLSFNALLESLSMKTVOGLSIQELVLSGNPLHCSC 178
QY 213 ---WIKOEVDIDIVOKTKVAGG---EIVRLIGGSAYVAPGASAIOMASYLKDRRWVY 266
DB 179 ALRWLGRMEBEG-----GGVPEQKLOCHGGGPLAHMPNMSC----- 215
QY 267 CSCYLOGGYGVONHYLGP-----CVIGRGVER-----IIELELTA 303
DB 216 -----GVPTLKQVNPNASVDVGDVLLRCQVGRGLEQAGWILTELEQSA 260

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## RESULT 15

US-08-440-816A-3  
 Sequence 3, Application US/08440816A  
 Patent No. 5914237

GENERAL INFORMATION:  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Mark, Melanie R.  
 APPLICANT: Sadick, Michael D.  
 APPLICANT: Shelton, David L.  
 APPLICANT: Wong, Wai Lee Tan  
 TITLE OF INVENTION: KINASE RECEPTOR ACTIVATION ASSAY  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 KB floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: pedit (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/440,816A

FILING DATE: 15-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/286305

FILING DATE: 05-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/170558

FILING DATE: 20-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/157563  
 FILING DATE: 23-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lee, Wendy M.  
 REGISTRATION NUMBER: 00,000  
 REFERENCE/DOCKET NUMBER: 854C1PIC3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1994  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 814 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-440-816A-3

Query Match 5.2%; Score 87; DB 2; Length 814;  
 Best Local Similarity 20.1%; Pred. No. 1.1;  
 Matches 71; Conservative 36; Mismatches 83; Indels 164; Gaps 17;

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QY 20 IGTMAFLCSLRELGDVDFVPMNPMKAMDISHNSSVVDIGITVYGSNSTECLKAD 79
DB 1 MGSTAA-----RLGAVILFVVI-----VGLHVGKRYAL--AD 31
QY 80 VVITAGITRKIPKSDKEMSRMDLFPNIMREVGAIKSYCPNMFVINITPLDVMA 139
DB 32 ASLKMDPNNFRGKD-----LPVLDQLLEVAAPCPDACCPCG----- 68
QY 140 ALOESSGLPHHRICGAGMLDSRF-----RRMIADKLEVSPRDYGM---- 182
DB 69 -----SSGLR-----CTRDGALDSLHLPGAENLTETYENQOHLQHEL--RDLRGLGELR 118
QY 183 -----VIGVHGDHWP--LSR-----YATVNCIPLSEYVKKG----- 212
DB 119 NLTIVKSGLRFPAPDAFHPTPLRLSLNLSFNALLESLSMKTVOGLSIQELVLSGNPLHCSC 178
QY 213 ---WIKOEVDIDIVOKTKVAGG---EIVRLIGGSAYVAPGASAIOMASYLKDRRWVY 266
DB 179 ALRWLGRMEBEG-----GGVPEQKLOCHGGGPLAHMPNMSC----- 215
QY 267 CSCYLOGGYGVONHYLGP-----CVIGRGVER-----IIELELTA 303
DB 216 -----GVPTLKQVNPNASVDVGDVLLRCQVGRGLEQAGWILTELEQSA 260

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Search completed: November 15, 2000, 09:47:18  
 Job time: 34 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2000, 09:46:44 : Search time 41.48 Seconds  
(without alignments)  
1078.393 Million cell updates/sec

Title: US-08-676-882-2

Perfect score: 1688

Sequence: 1 MAVREKMTNPRIAMVSGMT.....GSIDVEKMKAIALDASK 330

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 870496 seqs, 135550690 residues

Total number of hits satisfying chosen parameters: 870496

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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26: /cgn2\_6/ptodata/2/paa/US101.COMB.pep.\*  
27: /cgn2\_6/ptodata/2/paa/US102.COMB.pep.\*

\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	828	49.1	315	1	PCT-US98-18626-2
2	828	49.1	315	4	US-08-046-160-2
3	828	49.1	315	6	US-08-224-594-2
4	828	49.1	315	14	US-08-932-194-2
5	828	49.1	315	14	US-08-932-194A-2
6	706	41.8	329	13	US-08-838-418-2

7	641	38.0	325	18	US-09-450-969-1257	Sequence 7257, Ap
8	464	27.5	324	16	US-09-107-532-6486	Sequence 6486, Ap
9	426	25.2	318	14	US-08-134-000-4417	Sequence 4417, Ap
10	406	24.1	334	14	US-08-932-194-22	Sequence 22, Appl
11	406	24.1	334	27	US-60-238-331-75	Sequence 75, Appl
12	401.5	23.8	330	18	US-09-450-969-4667	Sequence 4667, Ap
13	400	23.7	331	14	US-08-932-194-23	Sequence 23, Appl
14	395.5	23.4	307	16	US-09-107-532-4274	Sequence 4274, Ap
15	395	23.4	330	14	US-08-932-194-21	Sequence 21, Appl
16	388	23.0	332	19	US-09-583-110-4591	Sequence 4591, Ap
17	384.5	22.8	338	13	US-08-827-356-3184	Sequence 3184, Ap
18	384.5	22.8	338	20	US-09-611-529-6846	Sequence 6846, Ap
19	371	22.0	381	21	US-60-212-664-505	Sequence 505, App
20	363	21.5	320	19	US-09-535-381-2	Sequence 2, Appl
21	362	21.4	332	21	US-60-167-217-21730	Sequence 17678, A
22	362	21.4	332	21	US-60-173-464-17678	Sequence 21578, A
23	362	21.4	332	21	US-60-191-637-21578	Sequence 17015, A
24	362	21.4	332	21	US-60-191-681-17015	Sequence 443, App
25	356	21.1	381	17	US-09-215-435-443	Sequence 311, App
26	356	21.1	381	21	US-60-069-957-311	Sequence 30493, A
27	353.5	20.9	351	21	US-60-191-637-30493	Sequence 8059, Ap
28	295	17.5	320	17	US-09-252-691-8059	Sequence 17740, A
29	284.5	16.9	336	21	US-60-167-217-17740	Sequence 17738, A
30	284.5	16.9	336	21	US-60-191-637-17738	Sequence 7133, Ap
31	279	16.5	312	27	US-60-215-161-7133	Sequence 238, App
32	273.5	16.2	304	20	US-09-634-238-238	Sequence 2221, Ap
33	260	15.4	347	21	US-60-167-324-2221	Sequence 1981, Ap
34	260	15.4	347	21	US-60-173-386-1981	Sequence 2212, Ap
35	260	15.4	347	21	US-60-175-871-2212	Sequence 2026, Ap
36	260	15.4	348	21	US-60-184-775-2026	Sequence 42567, A
37	257	15.2	347	21	US-60-191-637-42567	Sequence 2151, Ap
38	257	15.2	347	21	US-60-191-700-2151	Sequence 3, Appl
39	246.5	14.6	338	14	US-08-922-957-3	Sequence 11, Appl
40	240	14.2	338	16	US-09-160-911-11	Sequence 17253, A
41	238.5	14.0	338	17	US-09-248-796-17253	Sequence 17253, A
42	236.5	14.0	358	21	US-60-096-409-17253	Sequence 975, App
43	233	13.8	380	1	PCT-US00-05882-975	Sequence 4, Appl
45	231.5	13.7	298	14	US-08-922-957-4	

#### ALIGNMENTS

RESULT 1  
PCT-US98-18626-2  
Sequence 2, Application PC/TUS9818626  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
TITLE OF INVENTION: AND TREATING MALARIA  
NUMBER OF SEQUENCES: 20  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/18626  
FILING DATE: 08 SEPTEMBER 1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/932,194  
FILING DATE: 17 SEPTEMBER 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: REMILARD, JANE E.  
REGISTRATION NUMBER: 38,872  
REFERENCE/DOCKET NUMBER: DCI-103PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2000, 09:46:44 ; Search time 23.01 Seconds

(without alignments)  
1339.134 Million cell updates/sec

Title: US-08-676-882-2

Sequence: 1 MAVEKNTKRIAMVSGMT.....GSIDEVEMOKAIALDASK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP\_ARCHAEA:\*\*\*  
2: SP\_BACTERIA:\*\*\*  
3: SP\_FUNGI:\*\*\*  
4: SP\_HUMAN:\*\*\*  
5: SP\_INVERTEBRATE:\*\*\*  
6: SP\_MAMMAL:\*\*\*  
7: SP\_MHC:\*\*\*  
8: SP\_ORGANELLE:\*\*\*  
9: SP\_PHAGE:\*\*\*  
10: SP\_PLANT:\*\*\*  
11: SP\_PROTOZOA:\*\*\*  
12: SP\_VIRUS:\*\*\*  
13: SP\_VERTEBRATE:\*\*\*  
14: SP\_UNCLASSIFIED:\*\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1041.5	61.7	329	5 P90613	P90613 toxoplasma
2	808.5	47.9	316	10 P93052	P93052 botryococcus
3	634	37.6	324	2 O55383	O55383 synechocyst
4	605.5	35.9	335	2 O67655	O67655 aquifex aeo
5	569	34.7	334	2 O67581	O67581 aquifex aeo
6	451	26.7	338	5 O44340	O44340 styela plic
7	440.5	26.1	353	10 O49191	O49191 arabidopsis
8	440.5	26.1	353	10 O23569	O23569 arabidopsis
9	430.5	25.5	331	13 O93537	O93537 harpagifer
10	428.5	25.4	331	13 O93545	O93545 lepidonotol
11	428	25.4	317	2 O59244	O59244 bacillus ca
12	427.5	25.3	331	13 O93541	O93541 champsoceph
13	426.5	25.3	331	13 O93549	O93549 chionodraco
14	424.5	25.1	331	13 O93546	O93546 patagonotot
15	423.5	25.1	331	13 O9PRR8	O9PRR8 notochenta
16	422.5	25.0	331	13 O93539	O93539 notochenta
17	422.5	25.0	331	13 O93540	O93540 gobionototh
18	422	25.0	317	2 O9S0N0	O9S0N0 bacillus st
19	422	25.0	332	13 O93542	O93542 eleginops m

## ALIGNMENTS

20	422	25.0	332	13 O9PW58	O9PW58 rhizophila
21	421.5	25.0	331	13 O93538	O93538 paracheute
22	420	24.9	332	11 O64483	O64483 mus musculus
23	419.5	24.9	331	13 O93543	O93543 paraneotha
24	418	24.8	333	13 O93543	O93543 anguilla ro
25	415	24.6	332	13 O93401	O93401 coriophor
26	409.5	24.3	331	13 O93544	O93544 disostichu
27	409.5	24.3	331	13 O93544	O93544 disostichu
28	409	24.2	332	13 O93620	O93620 gillilichthys
29	407	24.1	332	13 O13276	O13276 sphyraena a
30	406	24.1	332	13 O13277	O13277 sphyraena a
31	406	24.0	332	13 O13278	O13278 sphyraena l
32	405.5	24.0	333	2 O32765	O32765 lactobacill
33	405	23.9	335	13 O9W7L4	O9W7L4 scelopor
34	404	23.9	333	13 O9W7M6	O9W7M6 amydistoma m
35	404	23.9	334	13 O9PVK4	O9PVK4 brachydania
36	404	23.8	333	10 O9ZKJ5	O9ZKJ5 oryza sativ
37	402	23.7	332	13 O9W5Z7	O9W5Z7 xenopus lae
38	400	23.7	332	6 O9XR87	O9XR87 monodelphis
39	400	23.7	334	6 O9YI05	O9YI05 squalus aca
40	399.5	23.7	350	10 O96569	O96569 lycoperis
41	399.5	23.6	331	13 P79912	P79912 scelopor
42	399	23.6	333	13 O9PT42	O9PT42 trachemys s
43	398	23.6	316	2 O51114	O51114 borrelia bu
44	398	23.6	332	13 P79913	P79913 scelopor
45	398	23.6	332	13 P79913	P79913 scelopor

RESULT 1	P90613	PRELIMINARY:	PRT: 329 AA.
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AC	P90613		
DT	01-MAY-1997 (TREMBLER, 03, Created)		
DT	01-MAY-1997 (TREMBLER, 03, Last sequence update)		
DT	01-MAY-2000 (TREMBLER, 13, Last annotation update)		
DE	LACTATE DEHYDROGENASE (EC 1.1.1.27) (L-LACTATE DEHYDROGENASE)		
DE	(LACTIC ACID DEHYDROGENASE)		
OS	Toxoplasma gondii.		
OS	Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;		
OC	Toxoplasma.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-ME49;		
RC	MEDLINE: 97169139.		
RA	Yang S., Parmley S.F.;		
RT	*Toxoplasma gondii expresses two distinct lactate dehydrogenase		
RT	homologous genes during its life cycle in intermediate hosts.*;		
RL	Gene 184:1-12(1997).		
CC	-I- CATALYTIC ACTIVITY: (S)-LACTATE + NAD(+) = PYRUVATE + NADH.		
DR	EMBL: U35118; AAC47443.1;		
DR	HSSP: 027743; ICER.		
DR	INTERPRO: IPR001236;		
DR	INTERPRO: IPR001557;		
DR	PFAM: PF000056; 1dh; 1.		
DR	PRINTS: PR00086; LLDHRCNASE.		
KW	Oxidoreductase.		
SEQUENCE	329 AA: 35548 MW: F06387B5AC0E6BBB CRC64:		
Query Match	61.7%: Score 1041.5; DB 5; Length 329;		
Best Local Similarity	60.4%: Pred. No. 3.3e-72;		
Matches 194; Conservative 55; Mismatches 71; Indels 1; Gaps 1;			
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DB	9 RKKVAMIGSGMGITMGYLCALRELADVLVYVKGMPGKALDISHNSVVDITNSVA 68		
QY	69 SWSYE-CLKGADVVITITGTTIKPKSDKESRMDDLVPVNTIMEVGAITSYCPNAFV 127		
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RL Mol. Biol. Evol. 14:1273-1284(1997).  
 CC -1- CATALYTIC ACTIVITY: (S)-LACTATE + NAD(+) = PYRUVATE + NADH.  
 DR EMBL: AF023168; AAC02943.1; -.  
 DR HSSP: P00339; 9LDB.  
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 DR PFAM: PF000056; 1db; 1.  
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 KW Oxidoreductase.  
 SQ SEQUENCE 338 AA; 36901 MW; A68DCE2756697F72 CRC64;

Query Match 26.7%; Score 451; DB 5; Length 338;  
 Best Local Similarity 32.2%; Pred. No. 6.7e-27;  
 Matches 106; Conservative 69; Mismatches 128; Indels 26; Gaps 8;

OY 6 KTRPKIAVWGSGMIGTMAFLCSLREL-GDVVLPDVPNPMKRAMDISHNSVVDTCI 64  
 DB 23 KSGPSKVTVYGVGVGMACMSVVLKGLCTDLVLDVVDKLOGEYMDLHSGSLFLE-NI 81  
 OY 65 TVYGSNSYECLKADVVIITAGITRKIPGSKDRKESRMDLLPVNIKIMREVGAIKSCYCN 124  
 DB 82 KYGGKDVSVANSNRIVITAGARQOPG-----SRLSLVQRNVNIFKHIIPOIATYSPS 136  
 OY 125 AFVINTNPDLVVAALQESSGLPHHRICGMAGMLDSSRFRMIADKLEVSPPDVGMVI 184  
 DB 137 ALLIVSNVVDLTVMYVAMKLSNFRNRVIGSGTNLDSARFRLIAEKLMLSPSYVHGWI 196  
 OY 185 GVHGHMVPLSRYATVNGIPLSEFVK-----GMIOEVDLIVQTKYAGG-EIYR 235  
 DB 197 GEHGDSSVMWMSGVNVCGLNSIHPRIGYPDGPEGM-----DKIHQVVDVGAADVIR 249  
 OY 236 LUGGSAAVYAPGASAIQMAESTYKDKRRVWVCSCYLOGGYVGNH-LGVPCVIGRGVE 294  
 DB 250 L-KQYTNMAIGLSCAELLATILHHRHRIHPVTCFVKGRKGIITDVCCLSPCLVLCNGVN 307  
 OY 295 KITELELTAQEROELGSGIDEVKEKOKAI 323  
 DB 308 SIYVNDLTFEEEMAIKKSMTIADYQKGL 336

RESULT 7  
 O49191 PRELIMINARY; PRT; 353 AA.  
 AC 049191;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE LACTATE DEHYDROGENASE (EC 1.1.1.27) (L-LACTATE DEHYDROGENASE)  
 DE (LACTIC ACID DEHYDROGENASE).  
 GN LDH1.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;  
 OC Brassicaceae; Arabidopsids.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, ECOTYPE C24;  
 RA Dolferus R., Peacock W.J., Dennis E.S.;  
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: (S)-LACTATE + NAD(+) = PYRUVATE + NADH.  
 DR EMBL: AF043130; AAC02678.1; -.  
 DR HSSP: P00339; 9LDB.  
 DR MENDEL: 28075; Arabid.1258;28075.  
 DR INTERPRO: IPR000205; -.  
 DR INTERPRO: IPR001236; -.  
 DR INTERPRO: IPR001557; -.  
 DR PFAM: PF000056; 1db; 1.  
 DR PRINTS: PR00086; LLDHRCNASE.  
 DR PROSITE: PS00064; L\_LDH; 1.  
 KW Oxidoreductase.  
 SQ SEQUENCE 353 AA; 37936 MW; 359FCD03CF31260E CRC64;

Query Match 26.1%; Score 440.5; DB 10; Length 353;  
 Best Local Similarity 32.8%; Pred. No. 4.6e-26;  
 Matches 106; Conservative 75; Mismatches 127; Indels 15; Gaps 7;

OY 7 NTRPKIAVWGSGMIGTMAFLCSLRELCD-VLFDVVPNPMKRAMDISHNSVVD-TGI 64  
 DB 38 NRRTKSVGVGVGMVIAIQTILTOLEADLALVDKPKLRGEMDLQHAFAFLPRTKI 97  
 OY 65 TVYGSNSYECLKADVVIITAGITRKIPGSKDRKESRMDLLPVNIKIMREVGAIKSCYCN 124  
 DB 98 T-ASVDYEVTAGSDLCITYAGARQNPGE-----SRLNLLQRNVNIFRHIIPPLAASPD 150  
 OY 125 AFVINTNPDLVVAALQESSGLPHHRICGMAGMLDSSRFRMIADKLEVSPPDVGMVI 184  
 DB 151 SILIVSNVVDLTVMYVAMKLSGFPNVRVIGSGTNLDSRFRFLIADHVNADVQATIV 210  
 OY 185 GVHGHMVPLSRYATVNGIPLSEFVKKMKIOPE--VDDIVQTKYAGEIYRLQGS 242  
 DB 211 GEHGDSSVALMSSISVGIVPLSFLEKNQIAVEKOTLEDIHQAVVGSAYEIGLKGYTS- 269  
 OY 243 YVAPGASAIQMAESTYKDKRRVWVCSCYLOGGYVGNH-LGVPCVIGRGVEKITELE 300  
 DB 270 -VAIGYSVANLARTILRDQRKIHPTVLARGFYGVGDGVFLSLPALGRNGVAVTNVH 328  
 OY 301 LTAQEROELGSGIDEVKEKOKAI 323  
 DB 329 MTDEAEKILKSAKTILEMOSQL 351

RESULT 8  
 O23569 PRELIMINARY; PRT; 353 AA.  
 AC 023569;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE LACTATE DEHYDROGENASE.  
 DE Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;  
 OC Brassicaceae; Arabidopsids.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 98121113.  
 RA Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,  
 RA Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,  
 RA Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,  
 RA Wedler E., Wambutt R., Weitzengruber T., Pohl T.M., Terryn N.,  
 RA Gjeien J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,  
 RA Auborg S., Gy I., Kreis H., Lao N., Kavanagh T., Hempel S., Kotler P.,  
 RA Ertlan K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,  
 RA Silvey M., James R., Montfort A., Pons A., Puigdomenech P., Douka A.,  
 RA Voukrelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B.,  
 RA Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,  
 RA Palmer K., Benes V., Rechman S., Ansoorge W., Cooke R., Berger C.,  
 RA Delseny M., Voet M., Volckaert G., Mewes H.W., Klosterman S.,  
 RA Schueller C., Chaiwalzais N.;  
 RT "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of  
 Arabidopsis thaliana."  
 RT Nature 391:485-488(1998).  
 DR EMBL: 297343; CAB10507.1; -.  
 DR HSSP: P00339; 9LDB.  
 DR MENDEL: 26784; Arabid.1258;26784.  
 DR INTERPRO: IPR000205; -.  
 DR INTERPRO: IPR001236; -.  
 DR INTERPRO: IPR001557; -.  
 DR PFAM: PF000056; 1db; 1.  
 DR PRINTS: PR00086; LLDHRCNASE.  
 DR PROSITE: PS00064; L\_LDH; 1.  
 KW Oxidoreductase.  
 SQ SEQUENCE 353 AA; 37950 MW; F8467FD4BC298F2E CRC64;

Query Match 26.1%; Score 440.5; DB 10; Length 353;  
Best Local Similarity 32.8%; Pred. No. 4.6e-26;  
Matches 106; Conservative 75; Mismatches 127; Indels 15; Gaps 7;

QY 7 NTRPKIAMVSCMGIMGMAFLCSLRELCD-VLPDVPNPMGKAMDISHSSVVD-TCI 64  
Db 38 NRRKRVSVGVGNMGMAIAQIILTDLADALADAKPDKRGEMLDQHAAPLPRTKI 97  
QY 65 TVYGSNSYECLGADVITITAGITIKIPKSKDEKSRMDLLPVNIKIMREVGAAIKSYCPN 124  
Db 98 T--ASVYETVAGSDLCITVAGARQNGE-----SRLLNLQRRNALPRHILPLAKASPD 150  
QY 125 AFYINITNPLDVMAALQESSGLPHHRICGAGMLDSSRRFRMIADKLEVSPPDVQGVNT 184  
Db 151 SILIYSNPVDLYTVAMKLSGFPVNRVLGSGTMDSSRFRFLIADHLIDVNAQVQAFIV 210  
QY 185 GVHGDHVPISRATVNGIPLSEFEVKKGWIKOE--VDDIVQKRVAGETVRLGQSSA 242  
Db 211 GEGHDSVALMSSISVGCIPVLSFLEKNQIAYEKOTLEDIHQAVVAGAYEYIGLKGYTS- 269  
QY 243 YVAPGASAIOMAESYLRKRRVWVSCYLOGGVQ--NHLYGVCYIGRGVEKITELE 300  
Db 270 -MAIGSVANLARTILMDQKIHVTVLARGFYVDDGQVPLSLPALLGRGVAVATNVH 328  
QY 301 LTRQERQELGSDIEVKEWQKAI 323  
Db 329 MTDEAEKLOKSAKTILEMOSOL 351

RESULT 9  
093537 PRELIMINARY; PRT; 331 AA.

AC 093537;  
DT 01-NOV-1998 (Tremblrel. 08, Created)  
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)  
DE LACTATE DEHYDROGENASE-A (EC 1.1.1.27).  
GN LDH-A.  
OS Harpagifer antarcticus.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;  
OC Percormorpha; Perciformes; Notothenioidel; Harpagiferidae; Harpagifer.  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=MUSCLE;  
RA Fields P.A.; Somero G.N.;  
RT "Hot spots in cold adaptation: lactate dehydrogenase-A (A4-LDH)  
orthologs of antarctic notothenioid fishes."  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF079820; AAC63278.1;  
DR HSSP: P00339; 9LDH.  
DR INTERPRO: IPR001236;  
DR INTERPRO: IPR001557;  
DR PFM: PF00056; 1dh; 1.  
DR PRINTS: PR00086; LLDHGRNASE.  
DR PROSITE: PS00064; L\_LDH; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 331 AA: 36180 MW: 795FAB8CAF8B7CAA CRC64;

Query Match 25.5%; Score 430.5; DB 13; Length 331;  
Best Local Similarity 31.1%; Pred. No. 2.4e-25;  
Matches 102; Conservative 70; Mismatches 127; Indels 29; Gaps 8;

QY 8 TRPKIAMVSCMGIMGMAFLCSLRELCD-VLPDVPNPMGKAMDISHSSVVDGITY 66  
Db 19 SRKRVTVYGVGNMGMAISILIKDLCDLAVMDKDKLGEVMDLQHSLSLKTIV- 77  
QY 67 YGSNSYECLGADVITITAGITIKIPKSKDEKSRMDLLPVNIKIMREVGAAIKSYCPNAF 126  
Db 78 -GOKDYSVTANSKVVAVTAGARQOEGE-----SRLLNLQRRNALPRHILPLAKASPD 131

QY 127 VINITNPLDVMAALQESSGLPHHRICGAGMLDSSRRFRMIADKLEVSPPDVQGVNT 186  
Db 132 LMVSNPVDILTYVAMKLSGFPVNRVLGSGTMDSSRFRFLIADHLIDVNAQVQAFIV 210  
QY 187 HGDHVPISRATVNGIPL-----SEFVKKGM--IKOEVDIVQKRVAGETVRL 236  
Db 192 HGDSSVPWMSGVNVAGVSLQMLNPOMGTGEGDGMKAIHKKEVVD-----GAYEYIKL 243  
QY 237 LGQSAVYAPGASAIOMAESYLRKRRVWVSCYLOGGVQNH-YLGVPCYIGRGVEK 295  
Db 244 KGYTS--WALGMSVADLVESITKNMKVHPVSTLVQGHGVKDEFLSPCVLQNSGLTD 301  
QY 296 IIEELTAERQELGSDIEVKEWQKAI 323  
Db 302 VIHMTLAKKEEKQYKSAETILMGQKEL 329

RESULT 10  
093545 PRELIMINARY; PRT; 331 AA.

AC 093545;  
DT 01-NOV-1998 (Tremblrel. 08, Created)  
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)  
DE LACTATE DEHYDROGENASE-A (EC 1.1.1.27).  
GN LDH-A.  
OS Lepidonotothen nudiifrons.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;  
OC Percormorpha; Perciformes; Notothenioidel; Nototheniidae;  
OC Lepidonotothen.  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=MUSCLE;  
RA Fields P.A.; Somero G.N.;  
RT "Hot spots in cold adaptation: lactate dehydrogenase-A (A4-LDH)  
orthologs of antarctic notothenioid fishes."  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF079828; AAC63286.1;  
DR HSSP: P00336; 5LDH.  
DR INTERPRO: IPR001236;  
DR INTERPRO: IPR001557;  
DR PFM: PF00056; 1dh; 1.  
DR PRINTS: PR00086; LLDHGRNASE.  
DR PROSITE: PS00064; L\_LDH; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 331 AA: 36214 MW: 73BE2B6AE327B08E CRC64;

Query Match 25.4%; Score 428.5; DB 13; Length 331;  
Best Local Similarity 31.7%; Pred. No. 3.5e-25;  
Matches 103; Conservative 68; Mismatches 131; Indels 23; Gaps 8;

QY 8 TRPKIAMVSCMGIMGMAFLCSLRELCD-VLPDVPNPMGKAMDISHSSVVDGITY 66  
Db 19 SRKRVTVYGVGNMGMAISILIKDLCDLAVMDKDKLGEVMDLQHSLSLKTIV- 77  
QY 67 YGSNSYECLGADVITITAGITIKIPKSKDEKSRMDLLPVNIKIMREVGAAIKSYCPNAF 126  
Db 78 -GOKDYSVTANSKVVAVTAGARQOEGE-----SRLLNLQRRNALPRHILPLAKASPD 131  
QY 127 VINITNPLDVMAALQESSGLPHHRICGAGMLDSSRRFRMIADKLEVSPPDVQGVNT 186  
Db 132 LMVSNPVDILTYVAMKLSGFPVNRVLGSGTMDSSRFRFLIADHLIDVNAQVQAFIV 210  
QY 187 HGDHVPISRATVNGIPL-----SEFVKKGM--IKOEVDIVQKRVAGETVRL 236  
Db 192 HGDSSVPWMSGVNVAGVSLQMLNPOMGTGEGDGMKAIHKKEVVD-----GAYEYIKL 243  
QY 237 LGQSAVYAPGASAIOMAESYLRKRRVWVSCYLOGGVQNH-YLGVPCYIGRGVEK 295  
Db 244 KGYTS--WALGMSVADLVESITKNMKVHPVSTLVQGHGVKDEFLSPCVLQNSGLTD 301  
QY 296 IIEELTAERQELGSDIEVKEWQKAI 323  
Db 302 VIHMTLAKKEEKQYKSAETILMGQKEL 329

QY 240 GSAVYAPGASAIOMAESYLRKRRVWVSCYLOGGVQNH-YLGVPCYIGRGVEKITE 298  
Db 247 TS--WALGMSVADLVESITKNMKVHPVSTLVQGHGVKDEFLSPCVLQNSGLTDVTH 304



**RA** Fields P.A., Somero G.N.: "Hot spots in cold adaptation: lactate dehydrogenase-A (A4-LDH)  
**RT** orthologs of antarctic nototheniid fishes."  
**RJ** Submitted (Jul-1998) to the EMBL/GenBank/DDbj databases.  
**RL** EMBL; AF079830; AAC63288.1.;  
**DR** HSSP; F00339; 9LDH.  
**DR** INTERPRO: IPR001236; -;  
**DR** INTERPRO: IPR001557; -;  
**DR** Pfam; PF00056; ldh; 1.  
**DR** PRINTS; PR00086; LDHDHGNASE.  
**DR** PROSITE; PS00064; L\_LDH; 1.  
**KW** Oxidoreductase.

**SQ** SEQUENCE 331 AA; 36142 MW; 45BF26DC3A03237E CRC64;

Query Match 25.1%; Score 424.5; DB 13; Length 331;  
Best Local Similarity 31.1%; Pred. No. 7e-25;  
Matches 102; Conservative 69; Mismatches 128; Indels 29; Gaps  
8;

**OY** 8 TRPKIAMVSGSIGGMAMFLCSLRGLD-VLFDDVPNPMKKAADISHNSVDPTGV 66  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
19 SSKSYLVGIVGVAGNASALSILKLCDCLAVDVMEKLGKVEDLHGSLFKTKTY- 77  
67 YSNSYECCAKADVVIITPAGITKICKOSKEMSRBDLLPVNKIKIREVGAAIKSCPNAF 126  
78 -CDKDYSTANRSKVYVVITGARQDE-----SRLLVQRNVNIKFPIIPNVKTSPCSI 131  
**OY** 127 VINITNPILDVVAALOEESGLRPNRICGMAGMIDSSRFRRMTADKLEVSPPDYGAVIGV 186  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
133 LMWVSNPDILTLYVMKLSGPFPHRVISGTVLDARFRNLGEKLNHLSPSCAHMIYGE 191  
**OY** 187 HDHNVPFSRYATVNGTLP-----SEFYKKG--IKOEVDDIYOKTKVAGEIYL 236  
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
192 HDDSVPSWGIVNAVGSLOGINPQMGTGEDENMKAIHKIEYD-----GAVEYIKL 243  
**OY** 237 LGCGAYVARGASALOAMESTLKDKRKRWVCSCYLCQQGYQN- YLGPVCYIGRGYEK 295  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
244 KGYTS-WAIGHSVADIVESTITKNHKHPYSTVLQGHHGVKDEVLSVPCVLGNSGLTD 301  
**OY** 296 ILLELTAEORELOGSDIDEVKEMOKAI 323  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
**DB** 302 VIHMFLMAEEKOVOKSAETLMGVOKEL 329

**RESULT 15**

**O9PRH8 PRELIMINARY: PRT: 331 AA.**

**ID O9PRH8:**  
**AC O9PRH8:**  
**DT 01-MAY-2000 (TREMBLrel. 13, Created)**  
**DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)**  
**DT 01-JUN-2000 (TREMBLrel. 14, last annotation updates)**  
**DE LACTATE DEHYDROGENASE-A (EC 1.1.1.27).**  
**GN LDH-A.**  
**OS Notothenia angustata (Rockcod), and**  
**OS Pagotchenia boreogrevinkii (Bald rockcod) (Trematomus boreogrevinkii),**  
**OC Euthariota, Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:**  
**OC Actinopterygii: Neopterygii: Teleostei: Euteleostei: Acanthopterygii;**  
**NC Percomorpha: Perciformes; Notothenioidei; Nototheniidae; Notothenia,**  
**N RN [1]**  
**SEQUENCE FROM N.A.**  
**RC TISSUE=WHITE MUSCLE;**  
**RA Marshall C.J., Fleming R.I.;**  
**RT "Cold adaptation in lactate dehydrogenases from antarctic fish.";**  
**RL Submitted (Jul-1999) to the EMBL/GenBank/DDbj databases.**  
**DR EMBL; AF170846; AAO48488.1.;**  
**DR EMBL; AF170846; AAO48486.1.;**  
**DR INTERPRO: IPR001236; -;**  
**DR INTERPRO: IPR001557; -;**  
**DR Pfam; PF00056; ldh; 1.**  
**DR PRINTS; PR00086; LDHDHGNASE.**  
**DR PROSITE; PS00064; L\_LDH; 1.**  
**KW Oxidoreductase.**  
**SQ SEQUENCE 331 AA; 36169 MW; 7CB80409CA0FDAE9 CRC64;**

Query Match 25.1%; Score 423.5; DB 13; Length 331;  
Best Local Similarity 31.1%; Pred. No. 8.4e-25;  
Matches 102; Conservative 69; Mismatches 128; Indels 29; Gaps 8;

QY 8 TRPKIAMVSGMIGTMAFLCSLRELD-VLFDVVPNMPMGKAMDISHNSVVDGITY 66  
DB 19 SRNKVTVVGVGMGMSAISILKDLCDLAMDVMDKLGEMDLQHGSLFKTKIV- 77  
QY 67 YGSNSYECLEKADVVIITAGITKIPGKSDKWSRMDLLPVNIKIMREVGAAIKSYCPNAF 126  
DB 78 -GDKDYSVTANSKVVVYTAGARQOEGE-----SRLNLVGRNVNIFKFIIPNIWYSPNCI 131  
QY 127 VINITPDLVMAALDESSGLPHHRICGAGMLDSSFRFRMIADKLEVSPPDVQGNVIGV 186  
DB 132 LMVVSNPVDLITVAMKLSGFPRRHRYVSGTND SARFRHLIGEKHLHPSSCHAWIIGE 191  
QY 187 HGDHMPPLSRVATVNGIPL-----SEFVKKGW--IKQEVDDIVQKTKVAGGEIVRL 236  
DB 192 HGDSVVPVMSGVAVAGVSLQGLNPOMGTGDDGEMWKAHKEVVD-----GAYEVYIKL 243  
QY 237 LGGGSAYVAFGASAIQMAESYLRDKRKRVNVCSCYLOGQYGVQNH-YLVGVCVIGRGVEK 295  
DB 244 KGYTS--WAIQMSVADLVEIINKMHKVVHVPSTLYQGMHGKDEVFLSVPCVLGNSGLTD 301  
QY 296 ILELELTAEQRELQGSIDEVKEKOKAI 323  
DB 302 VIIMTLKAEKEKOVOKSAETLMGVOKEL 329

Search completed: November 15, 2000, 09:47:45  
Job time: 61 sec

P00339 sus scrofa  
P42120 xenopus lae  
P56121 lactobacilli  
Q29563 vulpes vulp  
P42121 xenopus lae  
Q08349 archaeoglob  
P15629 rattus norv  
P16125 mus musculu  
P42123 rattus norv  
P19858 bos taurus  
P04642 rattus norv  
Q92055 fundulus he

## ALIGNMENTS

330 IALDASK EMOKA

GSIDEVKEMQNALH...

87993

Total number

Maximum Match 0%

Listing 11.3

to have a  
predicted by chance to being printed

Pred. No. is the number of the score distribution greater than or equal to the total score distribution.

## Description

```

RESULT      1
LDH_TOXGO   STANDARD:          PRT:          326 AA.
AC           027797:
DT           01-NOV-1997 (Rel. 35, Created)
DT           01-NOV-1997 (Rel. 35, Last sequence update)
DT           01-NOV-1997 (Rel. 35, Last annotation update)
DT           01-NOV-1997 (Rel. 35, Last annotation update) (LDH).
DE           L-LACTATE DEHYDROGENASE [EC 1.1.1.27] (LDH).
OS           Toxoplasma gondii.
OC           Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida; Sarcocystidae;
RN           Toxoplasma.
CC           (1)
RP           SEQUENCE FROM N.A.
RC           STRAIN-ME9:
RX           MEDLINE: 96123406.
RA           Yang S., Parmley S.F.;
RT           "A bradyzoite stage-specifically expressed gene of toxoplasma gondii
RL           encodes a polypeptide homologous to lactate dehydrogenase."
RT           Mol. Biochem. Parasitol. 73:291-294(1995); - PYRUVATE + NADH.
RT           MoI. Biochem. Parasitol. 73:291-294(1995); - PYRUVATE + NADH.
CC           CATALYTIC ACTIVITY: L-LACTATE + NAD(+) = PYRUVATE + NADH.
CC           PATHWAY: FINAL STEP IN ANAEROBIC GLYCOLYSIS.
CC           SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC           This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC           or send an email to license@lsb-sib.ch).
CC           EMBL: U23207; ANC46863.1;
DR           HSPB: 027743; ILDG
DR           INTERPRO: IPR001236;
DR           INTERPRO: IPR001557;
DR           PEAM: PF000086; ILDHGRNASE
DR           PRINTS: PS000064; L.LDH: FALSE_NEG.
DR           PROSITE: PS000064; L.LDH: FALSE_NEG.
KM           Oxidoreductase; NAD: Glycolysis.
FT           ACT_SITE 186
FT           (BY SIMILARITY).
FT           ACCEPTS A PROTON DURING CATALYSIS
SO           ACT_SITE 186
SEQUENCE     326 AA: 35307 MW; E692C95A81FC031E CRC64;
                Length 326;
Query Match       63.5%; Score 1072; DB 1;
Best local Similarity 62.6%; Pred. No. 1.5e-74; Indels 0; Caps
Matches 199; Conservative 56; Mismatches 63;
9 RPKIAMGSMIGCTMAFLCSIRELGAVLFEDVVPNNPMGKAMDISHNSSVYDTGITAYG 68
1 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
8 RKRIAMISGMIGCTMGTCVLERLADVLLFQVTVMGEMGRKLDDSOAKTSIADINVSYS 67
1 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
69 SNSECKLCAGDVVITITAGTTRIKPGSKDSKSRMDLLPVNIKITREVGAIKSYPNAFYI 128
1 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
68 ANQTEKINGSDVVITITAGLTRKVPKSKDKSWSRDLPLFNKKIRIEVAAGVKKCPLAFVI 127
1 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```



DB 309 LOGSIDEVEMOKA 322  
1- 1 : 1  
298 FDKSGAVAGLCEA 311

RESULT 3  
LDH1\_PLAFD  
ID LDH1\_PLAFD  
AC 027743: STANDARD: PRT: 316 AA.  
DT 01-NOV-1997 (Rel. 35 Created)  
DE 15-JUL-1999 (Rel. 35, Last sequence update)  
OS L-LACTATE DEHYDROGENASE (EC 1.1.1.27) (LDH-P)  
OC Plasmodium falciparum (isolate CDC / Honduras).  
RN Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
RP SEQUENCE FROM N.A.  
RC STRAIN=HONDURAS 1:  
RX MEDLINE: 93295434.  
RA Bzik D.J., Fox B.A., Gonyer K.;  
RT "Expression of Plasmodium falciparum lactate dehydrogenase in  
RL Escherichia coli.";  
RN Mol. Biochem. Parasitol. 59:155-166(1993).  
RP X-RAY CRYSTALLOGRAPHY (1.74 ANGSTROMS).  
RA Duun C., Banfield M., Barker J., Higham C., Moreton K.,  
RA Turgut-Balik D., Brady L., Holbrook J.J.;  
RT "The structure of lactate dehydrogenase from Plasmodium falciparum reveals a new target for anti-malarial design."  
RL Nat. Struct. Biol. 3:912-915(1996).  
CC -1 CATALYTIC ACTIVITY: L-LACTATE + NAD(+) = PYRUVATE + NADH.  
CC -1 PATHWAY: FINAL STEP IN ANAEROBIC GLYCOLYSIS.  
CC -1 SUBUNIT: HOMOTETRAMER.

-----  
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DR EMBL: M93720; AAA29633.1;  
DR PDB: 1LCG; 17-SEP-97.  
DR PDB: 1CBO; 19-MAR-99.  
DR DR INTERPRO: IPR001236;  
DR DR INTERPRO: IPR001557;  
DR PFAM: PF00036; 1dh; 1.  
DR PRINTS: PR00086; LLDHGNASE.  
DR PROSITE: PS00064; L\_LDH; FALSE\_NEG.  
KW Oxidoreductase; NAD; Glycolysis; 3d-structure.  
FT ACT\_SITE 182 182  
FT FT ACCEPTS A PROTON DURING CATALYSIS  
FT VARIANT 73 73 (BY SIMILARITY).  
FT VARIAT 96 96 A-> S.  
SQ SEQUENCE 316 AA; 34108 WT; D-> L.



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DR EMBL: 005257: AAA96343.1;  
DR EMBL: AF008220: AAC00347.1;  
DR EMBL: 299118: CAC14872.1;  
DR HSSP: 027743: 1LDG;  
DR SUBTILIST: BG11386; C17H;  
DR INTERPRO: IPR001236;  
DR INTERPRO: IPR001252;  
DR INTERPRO: IPR001557;  
PFAM: PF00056; 1dh; 1;  
PRINTS: PR00086; LLDHRCGNASE;  
DR PROSITE: PS00068; MDH; FALSE; NEG;  
KW Oxidoreductase; Tricarboxylic acid cycle; NAD;  
FT INIT\_MET 0  
FT ACT\_SITE 152 152 PROTON-RELAY (BY SIMILARITY);  
FT BINDING 155 155 SUBSTRATE CARBOXYL GROUP (BY SIMILARITY);  
FT ACT\_SITE 179 179 PROTON-RELAY (BY SIMILARITY);  
SQ SEQUENCE 311 AA; 33512 MW; 475287BFB852FB09 CRC64;

Query Match 43.8%; Score 740; DB 1; Length 311;  
Best Local Similarity 45.9%; Pred. No. 2.5e-49;  
Matches 147; Conservative 63; Mismatches 98; Indels 12; Gaps 3;

QY 7 NTRPKIAMVSGMIGGTAFGLCSLRELDGVVLFVY--VPNMGMKAMDISHNSVVDVGI 64  
DB 2 NTRKRVSYVIGAGFTGATTAFLAQLKELADVIVLIPOLENPKKALDMLKSPVQGEDA 61  
QY 65 TVYGSNSYECLEKADGVITITAGITKIPKSDKESRMDLVPNIKIMREYGAIRKSYCPN 124  
DB 62 KITGSNEYEDFADSDIVITAGIARKPG-----MSRDLVSTNEMKIMSVQEIYKSPD 116  
QY 125 AFVINTPLDVMVAALQESSGLPHHRTGCMAGMDSFRFMIDKLEVSPPDVQGMV 184  
DB 117 SIIVLNPVDMATYVYKESGPKRHRVIGSGVLDTAFRFPAVEELNLSKVDYTGFLV 176  
QY 185 GVHGDHVPPLSRATVNGIPLSEFVKKGMIOKEEVDIVQKTVAGGEVIRLLGGSSAY 244  
DB 177 GGHGDMVPLVRISYAGGIPLETILPK-----ERIDAIYERTKKGGEIVNLGNSAY 231  
QY 245 APGASAIOMAESYLKDRKRVWVSCYLOGGVONHYLGPVCIYGRGVEKIIIELELTAQ 304  
DB 232 AAPASLTFEMVAAILKDKORVLPJTAIVLEGEGYIGVPTIYGCNGLDQIIIELELTDY 291  
QY 305 EROLOGSIDEVKEMOKRIA 324  
DB 292 ERAOLNKSVESSVKVMKVL 311

RESULT 6  
MDH\_BACIS STANDARD: PRT; 312 AA.  
AC 059202;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE MALATE DEHYDROGENASE (EC 1.1.1.37).  
GN MDH;  
OS Bacillus israeli;  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/staphylococcus group; Bacillus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 96276423.  
RA Wyne S.A., Nicholls D.J., Scaven M.D., Sundaram T.K.;  
RT "Tetrameric malate dehydrogenase from a thermophilic Bacillus:  
cloning, sequence and overexpression of the gene encoding the enzyme  
RT and isolation and characterization of the recombinant enzyme";  
RL Biochem. J. 317:235-245(1996).

CC -1 CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE + NADH.  
CC -1 SUBUNIT: HOMOTETRAMER.  
CC -1 SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: X90527: CAA62129.1;  
DR HSSP: 027743: 1LDG;  
DR INTERPRO: IPR001236;  
DR INTERPRO: IPR001252;  
DR INTERPRO: IPR001557;  
PFAM: PF00056; 1dh; 1;  
PRINTS: PR00086; LLDHRCGNASE;  
DR PROSITE: PS00068; MDH; FALSE; NEG;  
KW Oxidoreductase; Tricarboxylic acid cycle; NAD;  
FT ACT\_SITE 153 153 PROTON-RELAY (BY SIMILARITY);  
FT BINDING 156 156 SUBSTRATE CARBOXYL GROUP (BY SIMILARITY);  
FT ACT\_SITE 180 180 PROTON-RELAY (BY SIMILARITY);  
SQ SEQUENCE 312 AA; 33648 MW; 64CE3BFB1B3C02D2 CRC64;

Query Match 43.2%; Score 729; DB 1; Length 312;  
Best Local Similarity 44.5%; Pred. No. 1.7e-48;  
Matches 141; Conservative 69; Mismatches 95; Indels 12; Gaps 3;

QY 9 RPKIAMVSGMIGGTAFGLCSLRELDGVVLFVY--VPNMGMKAMDISHNSVVDVGI 66  
DB 5 RKRISVIGAGFTGATTAFLAQLKELADVIVLIPOLENPKKALDMLKSPVQGEDA 64  
QY 67 YGSNSYECLEKADGVITITAGITKIPKSDKESRMDLVPNIKIMREYGAIRKSYCPN 126  
DB 65 IGTSEYEEFADSDIVITAGIARKPG-----MSRDLVSTNEMKIMSVQEIYKSPD 119  
QY 127 VINTNPLDVMVAALQESSGLPHHRTGCMAGMDSFRFMIDKLEVSPPDVQGMV 186  
DB 120 IIVLNPVDMATYVYKESGPKRHRVIGSGVLDTAFRFPAVEELNLSKVDYTGFLV 179  
QY 187 HGDHVPPLSRATVNGIPLSEFVKKGMIOKEEVDIVQKTVAGGEVIRLLGGSSAY 246  
DB 180 HGDDHVPPLVRISYAGGIPLETILPK-----ERLEAIYERTKKGGEIVNLGNSAY 234  
QY 247 GASAIOMAESYLKDRKRVWVSCYLOGGVONHYLGPVCIYGRGVEKIIIELELTAQ 306  
DB 235 AASLVEWEALVKDORVLPJTAIVLEGEGYIGVPTIYGCNGLDQIIIELELTDY 294  
QY 307 OROLOGSIDEVKEMOKRI 323  
DB 295 AALEKSAESVVRNMKAL 311

RESULT 7  
MDH\_BACIC STANDARD: PRT; 312 AA.  
AC 09X4K8;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE MALATE DEHYDROGENASE (EC 1.1.1.37).  
GN MDH;  
OS Bacillus thermodenitrificans;  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/staphylococcus group; Bacillus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN:00462;  
RA Williams R.A.D., Welch S.G., Alawadhi S.A.;  
RT "Properties and primary structure of a thermostable L-malate

Query Match	42.48	Score	715	DB	1	Length	312
Best Local Similarity	43.58	Pred. No.	2e-47				
Matches	138	Conservative	69	Mismatches	98	Indels	12
						Gaps	3

RESULT	8
MDH_CHLAV	
ID	MDH_CHLAV
AC	P80040;
DT	01-NOV-1991 (Rel. 20, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	MALATE DEHYDROGENASE (EC 1.1.1.37).
GN	MDH.
OS	Chloroflexus aurantiacus.
OC	Bacteria; Green non-sulfur bacteria; Chloroflexaceae group.
OC	Chloroflexaceae; Chloroflexus.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-J-10-FL;
RX	MEDLINE; 96241868.
RA	Systad B., Emmerhoff O., Sirevag R.;

```
DR HSSP: Q21143; 1LDG.  
DR INTERPRO: IPR001236; -  
DR INTERPRO: IPR001252; -  
DR INTERPRO: IPR001557; -
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Query Match	40.0%;	Score 676;	DB 1;	Length 309;
Best Local Similarity	43.8%;	Pred. No. 1.8e-44;		
Matches 141;	Conservative 55;	Mismatches 110;	Indels 16;	Gaps 3

RESULT	9	
MDH_CHLTE		
ID	MDH_CHLTE	STANDARD;
AC	P80039; P94677;	PRT; 310 AA



OY 68 GSNSEYCEKAGADVVITITAGTIPKSDKESRMDLIPVNIKIREVGAALIKSTCPNAFV 127  
 DB 60 GSNDAVDADSDVITITAGTIPKSPG-----MTBEDLTKMAGIVKEVTDNIMKSNPDI 114  
 OY 128 INTNPLDVVAALQESSGLPHHRICMAGMLDSSRRFRRIADKLESPDPVCGMIVGH 187  
 DB 115 IYVSNPLDINTHAAWRSGLPKFRVYGMAGVLDNAFRSTIANELGVSMODINACVLGSH 174  
 OY 188 GDHNPVLSRAVAVNGIPLSEEVKKGMIKOEVDIVOKTKVAGEIYRLGQGSAYYAPG 247  
 DB 175 GDAWVAVVYKTYVAGIPIISDL-----LPAETIDKLVERTNGCAELVEHLKQGSAPFSPG 229  
 OY 248 ASALQMAESYLDRKRVWCSCYLOGGYVONHYLGPVCGYGRGVEKITELETAOERO 307  
 DB 230 SSVEVVEVESIVDRKRVLCPCAVGLEGOYIGDKTFVGPVKLRNGVEQIYEIMLDQDLD 289  
 OY 308 ELQGSIDEVKEKOKAI 323  
 DB 290 LLOKSAKIVDENCML 305

## RESULT 11

MDH\_AERPE STANDARD: PRT: 313 AA.  
 AC 09YEAL:  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE MALATE DEHYDROGENASE (EC 1.1.1.37).  
 GN MDH OR APE0672.  
 OS Aeropyrum pernix.  
 OC Archaea: Crenarchaeota: Desulfurococcaceae: Desulfurococcaceae:  
 OC Aeropyrum.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K1:  
 RX MEDLINE: 99310339.  
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,  
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankaï A., Kosugi H.,  
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,  
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,  
 RA Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,  
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.:  
 RT "Complete genome sequence of an aerobic hyper-thermophilic  
 RT crenarchaeon, Aeropyrum pernix K1.";  
 RL DNA Res. 6:83-101(1999).  
 CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALACETATE + NADH.  
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.  
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 CC EMBL: AP000060; BAA79645.1;  
 DR INTERPRO: IPR001236;  
 DR INTERPRO: IPR001557;  
 DR PFM: PF00056; 1dh; 1.  
 DR PRINTS: PR00086; LDHHDGNASE.  
 DR PROSITE: PS00068; MDH; FALSE\_NEG.  
 KW Oxidoreductase; Tricarboxylic acid cycle; NAD.  
 FT ACT\_SITE 150 150 PROTON-RELAY (BY SIMILARITY).  
 FT BINDING 153 153 SUBSTRATE CARBOXYL GROUP (BY SIMILARITY).  
 FT ACT\_SITE 177 177 PROTON-RELAY (BY SIMILARITY).  
 SQ SEQUENCE 313 AA: 33984 MW: 7030040081772499 CAC64;

Query Match 33.2%; Score 560.5; DB 1; Length 313;  
 Best Local Similarity 35.9%; Pred. No. 1,le-35;

Matches 113; Conservative 72; Mismatches 119; Indels 11; Gaps 3;

OY 9 RPKIAYGSMIGCTMAFLCSRLRGDVLFDVYPNPKRADIISNSSVDTGITVYG 68  
 DB 4 QPLTTLTGAGGVGATVMTLMKRGYDLDLARTPCGPCEALDLAAHAAELGVDIRISG 63  
 OY 69 SNEYCEKAGADVITITAGTIPKSDKESRMDLIPVNIKIREVGAALIKSTCPNAFV 128  
 DB 64 SNEEDMRGSDIVLYTRGIGTRKPG-----MTREGLFANNTMAADLAEKIKAKADLIV 118  
 OY 129 INTNPLDVVAALQESSGLPHHRICMAGMLDSSRRFRRIADKLESPDPVCGMIVGH 188  
 DB 119 ITNPVDAWTVYVWKKTGFPRFVYIGFSGILDSARMAVYISQKLGVSFKVNAIVLGMHG 178  
 OY 189 DHNPVLSRAVAVNGIPLSEEVKKGMIKOEVDIVOKTKVAGEIYRLGQGSAYYAPGA 248  
 DB 179 OKMFPVPRLSVGVVPLEHLSK-----EEIEEVSETVNAGAKITELRGY-SSNYGPA 232  
 OY 249 SAIQMAESYLDRKRVWCSCYLOGGYVONHYLGPVCGYGRGVEKITELETAOERO 308  
 DB 233 GLVLTVEAIRDRSKRITPYSLILQGETGYNDIVAEVPAVIGKSIDERILPLEDEK 292  
 OY 309 LOGSIDEVKEKOKAI 323  
 DB 293 FDEAVQAVKKIVETL 307

## RESULT 12

LDH\_BACSU STANDARD: PRT: 320 AA.  
 AC P13714;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE L-LACTATE DEHYDROGENASE (EC 1.1.1.27).  
 GN LDH OR LGTE.  
 OS Bacillus subtilis.  
 OC Bacteria: Firmicutes: Bacillus/Clostridium group:  
 OC Bacillus/Staphylococcus group: Bacillus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-168:  
 RX MEDLINE: 97124189.  
 RA Yamane K., Kumano M., Kurita K.:  
 RT "The 25 degrees-36 degrees region of the Bacillus subtilis  
 RT chromosome: determination of the sequence of a 146 kb segment and  
 RT identification of 113 genes.";  
 RL Microbiology 142:3047-3056(1996).  
 RN [2]

RP SEQUENCE.  
 RX MEDLINE: 87076052.  
 RA Hediger M.A., Frank G., Zuber H.:  
 RT "Structure and function of L-lactate dehydrogenases from thermophilic  
 RT and mesophilic bacteria. IV. The primary structure of the mesophilic  
 RT lactate dehydrogenase from Bacillus subtilis.";  
 RL Biol. Chem. Hoppe-Seyler 367:891-903(1986).  
 CC -1- CATALYTIC ACTIVITY: L-LACTATE + NAD(+) = PYRUVATE + NADH.  
 CC -1- PATHWAY: FINAL STEP IN ANAEROBIC GLYCOLYSIS.  
 CC -1- SUBUNIT: HOMOTETRAMER.  
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 CC EMBL: D50453; BAA08939.1; ALT\_INIT.  
 DR EMBL: Z99105; CAB12099.1; ALT\_INIT.  
 DR PIR: A25805; A25805.  
 DR HSSP: P00344; 1LDB.  
 DR SUBTILIST; B619003; LDH.

DR INTERPRO: IPR001236; -  
 DR INTERPRO: IPR001557; -  
 DR PFAM: PF00056; 1db; 1.  
 DR PRINTS: PR00086; LLDHGRNASE.  
 DR PROSITE: PS00064; L\_LDH; 1.  
 KM Oxidoreductase; NAD; Glycolysis.  
 FT ACT\_SITE 178 178  
 FT CONFLICT 38 38  
 FT CONFLICT 51 51  
 FT CONFLICT 57 58  
 FT CONFLICT 120 120  
 FT CONFLICT 224 224  
 FT CONFLICT 315 318  
 FT CONFLICT 320 320  
 SEQUENCE 320 AA: 34786 MW: D2D9466A7329C95F CRC64;

Query Match 27.3%; Score 460; DB 1; Length 320;  
 Best Local Similarity 33.4%; Pred. No. 4.9e-28;  
 Matches 106; Conservative 69; Mismatches 124; Indels 18; Gaps 7;

QY 11 KIAYGSGMIGTMAFLCSLRELGD-VLEDDVPMNPMKAMDISHSSVDTGT---T 65  
 DB 7 KVALIGAGVGSVAFLINOGITDELIVDVNKEKAMDVMDLPHGKAF---GLQPVKT 63  
 QY 66 VYGSNVECLKAGADVITAGITRKIPKSDKEMSRMDLPVNIKIMREYGAIAKSCIPA 125  
 DB 64 SYG--TYEDCKADIVCIACAGANQPG-----TRLEVEKNKIKFPGIVSEVMAISGFDG 116  
 QY 126 FVINTNPLDVVAALQESSGLPHHRICGMAGMLDSRRFRRIADKLESPRDQCMVIG 185  
 DB 117 IFLVATNPVDILVTYATWFGSLGPKREYIGSGTLDASRRRPMLESEFGAARPNVAHITG 176  
 QY 186 VHGDMVPLSRATVNGIPLESEFKKG-WIKOEVDVIVOKTKVAGETVRLLGGSNAV 244  
 DB 177 EHGDELPMVSHANVAGVPSVSELVKNDAVKEDELQIVDDVKNAYHIIIE--KKATVY 234  
 QY 245 APGASAIMAESYTLKDRKRVWCSCYLOGOVQVONHYLGPCVIGRGVEKIELELTQ 304  
 DB 235 GVAMSLANITRAILNENSILTYSLDQYGDADVITGVPVNVNGIGAGITELNLNK 294  
 QY 305 EROELGSDIDEVKEKQK 321  
 DB 295 EKEQFLHSAGVLKNILK 311

RESULT 13  
 LDH\_BACME STANDARD; PRT; 318 AA.  
 ID LDH\_BACME  
 AC P00345;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE L-LACTATE DEHYDROGENASE (EC 1.1.1.27).  
 GN LDH.  
 OS Bacillus megaterium  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Bacillus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DSM 090;  
 RX MEDLINE: 88107005.  
 RA Waldvogel S., Weber H., Zuber H.;  
 RT "Structure and function of L-lactate dehydrogenases from thermophilic  
 RT and mesophilic bacteria. VII. Nucleotide sequence of the lactate  
 RT dehydrogenase gene from the mesophilic bacterium Bacillus megaterium.  
 RT Preparation and properties of a hybrid lactate dehydrogenase  
 RT comprising moieties of the B. megaterium and B. stearothermophilus  
 RT enzymes.";  
 RL Biol. Chem. Hoppe-Seyler 368:1391-1399(1987).  
 RN [2]  
 RP SEQUENCE.  
 RX MEDLINE: 88050100.  
 RA Stangl D., Wiederkehr F., Suter F., Zuber H.;

RT "Structure and function of L-lactate dehydrogenases from thermophilic  
 RT and mesophilic bacteria. V. The complete amino-acid sequence of the  
 RT mesophilic L-lactate dehydrogenase from Bacillus megaterium.";  
 RL Biol. Chem. Hoppe-Seyler 368:1157-1166(1987).  
 RN [3]

RP PRELIMINARY SEQUENCE.

RA Wiederkehr F.;

RL Thesis (1982), ETH Zurich, Switzerland.

CC -1- CATALYTIC ACTIVITY: L-LACTATE + NAD(+) = PYRUVATE + NADH.

CC -1- PATHWAY: FINAL STEP IN ANAEROBIC GLYCOLYSIS.

CC -1- SUBUNIT: HOMOTETRAMER.

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CC EMBL: M22305; AAA22566.1; -

DR PIR: S00133; DEBSIM.

DR HSP: P00344; 1LDB.

DR INTERPRO: IPR001236; -

DR INTERPRO: IPR001557; -

DR PFAM: PF00056; 1db; 1.

DR PRINTS: PR00086; LLDHGRNASE.

DR PROSITE: PS00064; L\_LDH; 1.

KM Oxidoreductase; NAD; Glycolysis.

FT ACT\_SITE 181 181

FT SEQUENCE 318 AA: 35035 MW: 17122190576E1485 CRC64;

Query Match 27.0%; Score 455; DB 1; Length 318;  
 Best Local Similarity 31.7%; Pred. No. 1.2e-27;  
 Matches 101; Conservative 79; Mismatches 123; Indels 16; Gaps 8;

QY 4 FEKNRPKIAMVSGMIGTMAFLCSLRELGD--DVLEDDVPMNPMKAMDISHSSVY 60  
 DB 5 FLPKTR-KVAIVGTIGVGSYAF--SMVNOGTANLEVLIDMKKEAEGARIDNHGMPA 61  
 QY 61 DTGIVYGSNSYECLEKAGDVITAGITRKIPKSDKEMSRMDLPVNIKIMREYGAIAK 120  
 DB 62 -TPMKIWDGYKDC-ADADLAVITAGANQAPG-----TRLDVEKNVVFICFYKIDYN 114  
 QY 121 YCPNMFVINTNPDLVVAALQESSGLPHHRICGMAGMLDSRRFRRIADKLESPRDQ 180  
 DB 115 SGFDGILLVATNPVDILAVHTQKVSGLPMGRVYIGSGTILDTAFRYLLSDYFEDSRNVH 174  
 QY 181 GAVTGVGHMVPPLSRVATVNGIPLESEFKKGWIKOE-EVDDIVOKTKVAGETVRLLGQ 239  
 DB 175 AIMEHGTETPEPWSHAOIGVKEHFIINTAITEKEPOMHLEFOTRDAAYHIIIN--RK 232  
 QY 240 GSAVYAPGASAIOMAESYTLKDRKRVWCSCYLOGOVQVONHYLGPCVIGRGVEKIELE 299  
 DB 233 GATYGGIANGLVITRKAILDDENSILTYVALLEGYISDVYIGVPAIINKGVQIIEI 292  
 QY 300 ELTAEROELOSDIDEVKE 318  
 DB 293 NLTPHQDLHSASILKQ 311

RESULT 14  
 LDHP\_BACPS STANDARD; PRT; 318 AA.  
 ID LDHP\_BACPS  
 AC P14561;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-AUG-1991 (Rel. 19, Last annotation update)  
 DE L-LACTATE DEHYDROGENASE P (EC 1.1.1.27).  
 GN LCTA OR LDHP.  
 OS Bacillus psychrosaccharolyticus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;



```

OC Bacillus/Staphylococcus group: Bacillus.
RN [1]
RE SEQUENCE FROM N.A.
RX MEDLINE: 90241471.
RA Vekovski V., Schlatter D., Zuber H.;
RT "Structure and function of L-lactate dehydrogenases from
RT thermophilic, mesophilic and psychrophilic bacteria, IX.
RT identification, isolation and nucleotide sequence of two L-lactate
RT dehydrogenase genes of the psychrophilic bacterium Bacillus
RT psychrosaccharolyticus."
RL Biol. Chem. Hoppe-Seyler 371:103-110(1990).
RN [2]
RP SEQUENCE.
RX MEDLINE: 88134573.
RA Schlatter D., Kriech O., Suter F., Zuber H.;
RT "The primary structure of the psychrophilic lactate dehydrogenase
RT from Bacillus psychrosaccharolyticus."
RL Biol. Chem. Hoppe-Seyler 368:1435-1446(1987).
CC -1- CATALYTIC ACTIVITY: L-LACTATE + NAD(+) -> PYRUVATE + NADH.
CC -1- PATHWAY: FINAL STEP IN ANAEROBIC GLYCOLYSIS.
CC -1- SUBUNIT: HOMOTETRAMER.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X55118; CAA38914.1;
CC PIR: S08182; S08182.
CC HSSP: P00344; ILDB.
CC INTERPRO: IPR001236;
CC INTERPRO: IPR001557;
CC PFAM: PF00056; Idb: 1.
CC PRINTS: PR00086; LLDHRCNASE.
CC PROSITE: PS00064; L_LDH; 1.
CC Oxidoreductase; NAD: Glycolysis; Multigene family.
CC ACT_SITE 179
CC BY SIMILARITY.
CC SEQUENCE 318 AA; 35249 MW; F69165A3408E442A CRC64;

```

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LDH_THEMA
ID LDH_THEMA STANDARD: PRT: 319 AA.
AC P16115.
DT 01-APR-1990 (Rel. 14, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE L-LACTATE DEHYDROGENASE (EC 1.1.1.27).
GN LDH OR TMI867.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-MSB8 / DSM 3109;
RX MEDLINE: 94009031.
RA Ostendorp R., Liebl W., Schurig H., Jaenicke R.;
RT "The L-lactate dehydrogenase gene of the hyperthermophilic bacterium
RT Thermotoga maritima cloned by complementation in Escherichia coli.";
RL Eur. J. Biochem. 216:709-715(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-MSB8 / DSM 3109;
RX MEDLINE: 99287316.
RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
RN [3]
RP SEQUENCE OF 1-31.
RX STRAIN-MSB8 / DSM 3109;
RX MEDLINE: 90201029.
RA Wda A., Jaenicke R., Huber R., Stetter K.O.;
RT "Lactate dehydrogenase from the extreme thermophile Thermotoga
RT maritima.";
RL Eur. J. Biochem. 188:195-201(1990).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE: 98322364.
RA Auerbach G., Ostendorp R., Prade L., Kordorfer I., Dams T., Huber R.,
RA Jaenicke R.;
RT "Lactate dehydrogenase from the hyperthermophilic bacterium
RT Thermotoga maritima: the crystal structure at 2.1-A resolution
RT reveals strategies for intrinsic protein stabilization.";
RL Structure 6:769-781(1998).
CC -1- CATALYTIC ACTIVITY: L-LACTATE + NAD(+) -> PYRUVATE + NADH.
CC -1- PATHWAY: FINAL STEP IN ANAEROBIC GLYCOLYSIS.
CC -1- SUBUNIT: HOMOTETRAMER.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X74302; CAA52355.1;
CC EMBL: AE001823; AAD36929.1;
CC PIR: S36863; S36863.
CC PDB: 1A5Z; 23-MAR-99.
CC TIGR: TMI867.
CC INTERPRO: IPR001236;
CC INTERPRO: IPR001557;
CC PFAM: PF00056; Idb: 1.
CC PRINTS: PR00086; LLDHRCNASE.
CC PROSITE: PS00064; L_LDH; 1.
CC Oxidoreductase; NAD: Glycolysis; 3D-structure.
CC ACT_SITE 172
CC BY SIMILARITY.
CC CONFLICT 14 14 MISSING (IN REF. 3).

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A:Experimental source: strain K1  
C:Genetics:  
A:Gene: APE0672  
C:Superfamily: L-lactate dehydrogenase

Query Match 33.2%; Score 560.5; DB 2; Length 313;  
Best Local Similarity 35.9%; Pred. No. 1.2e-35;  
Matches 113; Conservative 72; Mismatches 119; Indels 11; Gaps 3;

OY 9 RPKIAMVSGMIGTAMFLCSRELGDVLPDVNPMFGKAMDISHNSVVDGTITVYG 68  
Db 4 OPLTIIIGAGVGMATVAMLMKGYDDLIIARTPGKPGEGALDLAHAAELGVDIRISG 63  
OY 69 SNSSECLGADVITTAGITIPGSKDEMSMDLPVNIKIMREVGAIISYCNNAVY 128  
Db 64 SNSIEDMGSDIVLTATGIRKPG-----MTREQLLENNANTMALAEKIAVYADALV 118  
OY 129 NITNPLDVVAALQSSGLPHHRICGMAGMLDSSRRFRIADKLEVSPPDVQGVYIGV 188  
Db 119 ITTNPDVDMYVVMKKTKGFPREVRVIGSGILDSAMAYIISQKLGVSFKSVAYILGHHG 178  
OY 189 DHMPLSRATVNGIPLSEFVKKGKIKOEVDIVQKTKVAGGELVRLLOGGSAYVAPGA 248  
Db 179 OKMEVPLRSSVGVPLRHLMSK-----EIEIEVVSFTVNAKITELRGY-SSNVCPPAA 232  
OY 249 SAIGMAESYLDRKRKRVAVSCYLOGGVGNHYIGVPCVIGRGVEKITELETOEHOE 308  
Db 233 GLVLVEIAIKRDSKRIYIYSLYLOGEYVNDIVAEVPAVIGSGIERLIELPLEDEKRR 292  
OY 309 LOGSIDEVKEKOKAI 323  
Db 293 FDEAVQAVKKLIVETL 307

## RESULT 8

E69649

L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000  
C:Accession: E69649; A25805

R:Kunst, P.; Ogatawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
C.; Bron, S.; Broillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fume, S.; Gallizi, A.; Gall  
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols,  
A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y., M.; Ogawa, K.; Ogatawara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portellell  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,  
A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot  
A.; Authors: Schlögl, M.; Tanaka, T.; Terstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033  
A:Accession: E69649

A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA

A:Residues: 1-321 <KUN>  
A:Cross-references: GB:299105; GB:AL009126; NID:92632457; PIDN:CAH12099.1; PID:92632591  
A:Experimental source: strain 168  
R:Heidiger, M.A.; Frank, G.; Zuber, H.  
Biol. Chem. Hoppe-Seyler 367, 891-903, 1986  
A:Title: Structure and function of L-lactate dehydrogenases from thermophilic and mesophil  
A:Reference number: A25805; MUID:97076052  
A:Accession: A25805  
A:Molecule type: protein  
A:Residues: 2-38, 'L', '40-51', 'N', '53-57', 'AP', '60-120', 'I', '122-224', 'T', '226-315', 'VN' <HED>  
C:Genetics:  
A:Gene: lctE  
C:Function:

A:Description: catalyzes the reversible oxidation of (S)-lactate to pyruvate by NAD+  
C:Superfamily: L-lactate dehydrogenase  
C:Keywords: NAD: oxidoreductase  
F:2-321/Product: L-lactate dehydrogenase #status experimental <MAT>  
F:8-38/Region: beta-alpha-beta NAD nucleotide-binding fold  
F:152,179/Active site: Asp, His #status predicted

Query Match 27.3%; Score 460; DB 2; Length 321;  
Best Local Similarity 33.4%; Pred. No. 6.2e-28;  
Matches 106; Conservative 69; Mismatches 124; Indels 18; Gaps 7;

OY 11 KIAMVSGMIGTAMFLCSRELGDVLPDVNPMFGKAMDISHNSVVDGTITVYG 65  
Db 8 KVALGAGVGSVYAFALINQGITDELVIDVKKAMQDVLDLPHGAF--GLQPKYT 64  
OY 66 VYGSNSYCLKADADVITTAGITIPGSKDEMSMDLPVNIKIMREVGAIISYCNNA 125  
Db 65 SVG--TYEDCKADADLVICACANQKPG-----TLELVKRLKIFKGVSVMASSFGDC 117  
OY 126 FVITNPLDVVAALQSSGLPHHRICGMAGMLDSSRRFRIADKLEVSPPDVQGVYIG 185  
Db 118 IFVATNPVDILTITVTKFSGLPKREVRVIGSGITLDSARFRLSEYFGAAPQVNAHIIIG 177  
OY 186 VHGDHMPLSRATVNGIPLSEFVKKG-WIKOEVDIVQKTKVAGGELVRLLOGGSAYV 244  
Db 178 EHGDELPLVMSHANGVAVSELEKNDAYKOEELDQIVDDKNAAYHIE--KKGATY 235  
OY 245 APGASAIOMAESYLDRKRKRVAVSCYLOGGVGNHYIGVPCVIGRGVEKITELETOE 304  
Db 236 GVAMSLARITKAILHNENSILVSTYLDQYIGADVYIGVAVVNRGSIAGITTELINKE 295  
OY 305 EROELGSDIDEVKEKOK 321  
Db 296 EKEQFLHSAGVKNILK 312

## RESULT 9

DEBSUM

L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus megaterium  
C:Species: Bacillus megaterium  
C:Date: 03-Aug-1984 #sequence\_revision 30-Sep-1991 #text\_change 11-Jun-1999  
C:Accession: S00133; S01472; A00354

R:Widvogel, S.; Weber, H.; Zuber, H.  
Biol. Chem. Hoppe-Seyler 360, 1391-1399, 1987  
A:Title: Structure and function of L-lactate dehydrogenases from thermophilic and mes  
megaterium. Preparation and properties of a hybrid lactate dehydrogenase comprising  
A:Reference number: S00133; MUID:88107005  
A:Accession: S00133  
A:Molecule type: DNA  
A:Residues: 1-318 <NAL>  
A:Cross-references: EMBL:M22305; NID:9143135; PIDN:AAA22566.1; PID:9143136  
R:Stangl, D.; Wiedekehr, F.; Suter, F.; Zuber, H.  
Biol. Chem. Hoppe-Seyler 366, 1157-1166, 1987  
A:Title: Structure and function of L-lactate dehydrogenases from thermophilic and mes  
terium.  
A:Reference number: S01472; MUID:88050100  
A:Accession: S01472  
A:Molecule type: protein  
A:Residues: 1-318 <STY>  
A:Comment: This enzyme is activated by fructose-1,6-diphosphate.  
C:Function:

A:Description: catalyzes the reversible oxidation of (S)-lactate to pyruvate by NAD+  
C:Superfamily: L-lactate dehydrogenase  
C:Keywords: homotetramer; NAD: oxidoreductase  
F:1-318/Product: L-lactate dehydrogenase #status experimental <MAT>  
F:11-41/Region: beta-alpha-beta NAD nucleotide-binding fold  
F:154,181/Active site: Asp, His #status predicted

Query Match 27.0%; Score 455; DB 1; Length 318;  
Best Local Similarity 31.7%; Pred. No. 1.5e-27;  
Matches 101; Conservative 79; Mismatches 123; Indels 16; Gaps 8;

L-lactate dehydrogenase (EC 1.1.1.27) - Thermotoga maritima (strain MSB)

C:Species: Thermotoga maritima

C:Date: 22-Jan-1994 #sequence\_revision 01-Dec-1995 #text\_change 18-Jun-1999

C:Accession: S36863; S36864; D72202

R:Ostermeyer, R.; Liebl, W.; Schurig, H.; Jaenicke, R.

Eur. J. Biochem. 216, 709-715, 1993

A:Title: The L-lactate dehydrogenase gene of the hyperthermophilic bacterium Thermotoga

A:Reference number: S36863; MUID:94009031

A:Accession: S36863

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-319 <OST>

A:Cross-references: EMBL:X74302; NID:9396280; PIDN:CAA52355.1; PID:9396281

A:Accession: S36864

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-31,38-53,55-85,163-173 <OS2>

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A72200; MUID:99287316

A:Accession: D72202

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-319 <ARP>

A:Cross-references: GB:AE001823; GB:AE000512; NID:94982441; PID:94982452; TIGR:TM1867

A:Experimental source: strain MSB

A:Gene: TM1867

A:Genetics:

C:Superfamily: L-lactate dehydrogenase

C:Keywords: oxidoreductase

Query Match 26.0%; Score 439.5; DB 2; Length 319;

Best Local Similarity 33.2%; Pred. No. 2.3e-26;

Matches 106; Conservative 64; Mismatches 134; Indels 15; Gaps 7;

QY 11 KIAMVSGMIGTMAFLCSLRELG-DVVLFDVVPMPMKAMDISHNSVDGTITVGS 69

DB 2 KIGIVGLGRVGSSTFALMKGFAREVLIIDPKRAEGDLDLHGTFETRA-NIT-A 59

QY 70 NSYELKAGADVITAGITKIPKSKDKEMSRDILLPVNIKIREVGAIAKSCPNAYIN 129

DB 60 GDVADLKSDVIVAAVAGVQKPGG---TRQLLLGRNARVKEIARNVSKYAPDSIVIV 114

QY 130 ITNPLDVVAALQESSGLPHRIGCMAGMLDSSFRPMIADKLEVSPPDVGVGIVGCD 189

DB 115 VTNPDVLTFFELKESGMDPRKVGSGVLDPAKRLTILAOHCSPSVHYVIGEHED 174

QY 190 HMVPLSRATVNGIPLS---EFVKKGIKEEVDIVOKTVAGGEIVRLLOGSAYYAP 246

DB 175 SEVPWSGAMIGIPIQNMQICQK-CDSKILENFAEKTRAAVEIIE--RKGNTHAI 230

QY 247 GASAIQMAESTYIAKDKRRVWCSYLOGGYQVNHLYGPCVIGGVEKIIELETAQER 306

DB 231 ALAAVDIVESTFPEKRVLTLSVYLEDYGVKLCISVPLVGLKHGVERIETLNEBEL 290

QY 307 QELQSIDVYKEMOKAIA 325

DB 291 EAFKRSASILKNAINEITA 309

#### RESULT 13

H64250

L-lactate dehydrogenase (EC 1.1.1.27) - Mycoplasma genitalium

C:Species: Mycoplasma genitalium

C:Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 07-Dec-1999

C:Accession: H64250

R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.

M.; Fuhmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.

C.A.; Venter, J.C.

Science 270, 397-403, 1995

A:Title: The minimal gene complement of Mycoplasma genitalium.

A:Reference number: A64200; MUID:96026346

A:Accession: H64250

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-312 <TIG>

A:Cross-references: GB:U39733; GB:LA3967; NID:91046177; PIDN:AAB01650.1; PID:91046180

A:Experimental source: strain G-37

C:Genetics:

A:Gene code: SGC3

C:Superfamily: L-lactate dehydrogenase

C:Keywords: oxidoreductase

Query Match 25.7%; Score 434.5; DB 2; Length 312;

Best Local Similarity 34.2%; Pred. No. 5.4e-26;

Matches 107; Conservative 63; Mismatches 128; Indels 15; Gaps 8;

QY 10 PKIAMVSGMIGTMAFLCSLRELG-DVVLFDVVPMPMKAMDISH-NSVDGTITVY 67

DB 4 PKIAIVGSGAVGTSPLYAAMTRALGSEYMIIDINEKAKGVNFDLQDASSCPNRYVA 63

QY 68 GSNSEYELKAGADVITAGITKIPKSKDKEMSRDILLPVNIKIREVGAIAKSCPNAY 127

DB 64 G-EYSQKLDYDFEFISAG---RPQKQGE-TRQLLEGVETIMKSIAREIKKSGFNGVT 117

QY 128 ITNPLDVVAALQESSGLPHRIGCMAGMLDSSFRPMIADKLEVSPPDVGVGIVG 187

DB 118 LIASNPVDIMSTYTLKVTGEPKPKVIGSGTLDSARLRAIARKYOMSSKDVQAYYIGEH 177

QY 188 GDMVPLSRATVNGIPLSEFVKKGIKEE-EVDIVOKTVAGGEIVRLLOGSAYY 245

DB 178 GDSVSIISSAKIAGLSLHFKASDIKEKEFEIDPFIRRAY---ETIE--RKGNFTYG 232

QY 246 PGASAIQMAESTYIAKDKRRVWCSYLOGGYQVNHLYGPCVIGGVEKIIELETAQ 305

DB 233 IEASADVAEQLIKDKTEVRVVAFLPTGQYAKMDMFGTPCVLSRGIKIIEIESTNE 292

QY 306 ROELQSIDVYKEMOKAIA 318

DB 293 KVALENSIKVVKD 305

#### RESULT 14

DELBLA

L-lactate dehydrogenase (EC 1.1.1.27) - Lactobacillus casei

C:Species: Lactobacillus casei

C:Date: 18-Apr-1984 #sequence\_revision 31-Dec-1993 #text\_change 07-Feb-1997

C:Accession: A43944; J00280; A00352

R:Kim, S.F.; Baek, S.J.; Pack, M.Y.

Appl. Environ. Microbiol. 57, 2413-2417, 1991

A:Title: Cloning and nucleotide sequence of the Lactobacillus casei lactate dehydroge

A:Reference number: A43944; MUID:92117575

A:Accession: A43944

A:Molecule type: DNA

A:Residues: 1-326 <KIM>

A:Experimental source: strain ATCC 393

A>Note: sequence extracted from NCBI backbone (NCBI:77578, NCBI:77579)

R:Taguchi, H.; Ohta, T.

submitted to JIPID, November 1991

A:Reference number: J00280

A:Accession: J00280

A:Molecule type: DNA

A:Residues: 2-326 <TAG>

A:Experimental source: strain ATCC393

R:Hensel, R.; Mayr, U.; Yang, C.

Eur. J. Biochem. 134, 503-511, 1983

A:Title: The complete primary structure of the allosteric L-lactate dehydrogenase fro

A:Reference number: A00352; MUID:83287369

A:Accession: A00352

A:Molecule type: protein

A:Residues: 2-25, 'F', 27-51, 'T', 53-87, 'KQ', 90-118, 'L', 120-269, 'I', 271-272, 'L', 274-326

C:Genetics:  
A:Gene: l-ict  
C:Function:  
A:Description: catalyzes the reversible oxidation of (s)-lactate to pyruvate by NAD+  
C:Superfamily: L-lactate dehydrogenase  
C:Keywords: homotetramer; NAD; oxidoreductase  
F:2-326/Product: L-lactate dehydrogenase #status experimental <MAT>  
F:11-41/Region: beta-alpha-beta NAD nucleotide-binding fold  
F:154,101/Active site: Asp, His #status predicted

Query Match 25.6%; Score 431.5; DB 1; length 326;  
Best Local Similarity 29.9%; Pred. No. 9.7e-26;  
Matches 96; Conservative 82; Mismatches 132; Indels 11; Gaps 6;

OY 1 MAVFEKNTPRKIAMVSGMIGTMAFLCSLRELG-DVVLFDVPPMPKAMDISHNSY 59  
DB 1 MASTIDKHOKVILVGDGAGSVAYANVLGIAOELGIVDFPKTKGDAIDLS-NALP 59  
OY 60 VDTGITVYSGNSYECLKAGADVITITAGITIKPKSDKESRMDLPVNIKIREVGAIR 119  
DB 60 FTSPKRIY-SAEYSDAKDADLVITAGAPKRG-TRLDLVNKNKLIKSTVDPY 113  
OY 120 SYCPRAFYINTNPDLVVAALQESSGLPHRIGCMAGMLDSSRRRMIAADKLEVSPPDY 179  
DB 114 DSGFNGITLVANPVDILTATATWKLKSGPKNRVSGSTLDTARFROSIAEMVNVDAARV 173  
OY 180 QGVNIGVGDHVPPLSRATVNGIPLSEFVK-KGMIOEVDIVQKTRVAGGEIVRLIG 238  
DB 174 HAYIMGEHDTPEFPMWAMNIGCVITAEVKAHPEIKEDLVKMFEDVDAAYETIKL-- 231  
OY 239 QGSAYAPGASAIQMAESYLDRKRVMWCYLOGGVONHYLGPVYIGRGVEKITE 298  
DB 232 KGATFYGIATLARIKALINDENAVLPSVMDQGYGINDIYICTPAVINNGIONILE 291  
OY 299 LETRAOEKOELOGSIDEVKEK 319  
DB 292 TPLTDEESMOKSASOLKVV 312

## RESULT 15

S08183  
L-lactate dehydrogenase (EC 1.1.1.27) X - Bacillus psychrosaccharolyticus  
C:Species: Bacillus psychrosaccharolyticus  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 14-May-1993  
C:Accession: S08183; A38031  
R:Vckovski, V.; Schlatter, D.; Zuber, H.  
Biol. Chem. Hoppe-Seyler 371, 103-110, 1990  
A:Title: Structure and function of L-lactate dehydrogenases from thermophilic, mesophilic  
and psychrophilic bacterium Bacillus psychrosaccharolyticus.  
A:Reference number: S08182; MUID:90241471  
A:Accession: S08183  
A:Status: not compared with conceptual translation.  
A:Molecule type: DNA  
A:Residues: 1-319 <VCK>  
A:Accession: A38031  
A:Molecule type: protein  
A:Residues: 1-24 <SCH1>  
C:Superfamily: L-lactate dehydrogenase  
C:Keywords: homotetramer; NAD; oxidoreductase  
F:1-319/Product: L-lactate dehydrogenase X #status experimental <MAT>

Query Match 25.5%; Score 431; DB 2; length 319;  
Best Local Similarity 31.4%; Pred. No. 1e-25;  
Matches 99; Conservative 76; Mismatches 122; Indels 18; Gaps 9;

OY 11 KIAMGSMIGCTMAFLC---SLRELGDVLFEDVPPMPKAMDISHNSYVDGCI-TV 66  
DB 8 RVALIGAGSVSSYAFALNOSTE--ELVITDVNEDKAMGDANDLNKGFAPNPTKW 65  
OY 67 YGSNSYECLKAGADVITITAGITIKPKSDKESRMDLPVNIKIRE-VGAIRKSYCPNA 125  
DB 67 YGSNSYECLKAGADVITITAGITIKPKSDKESRMDLPVNIKIRE-VGAIRKSYCPNA 125

DB 66 YG--NYDDCKEADIVICAGANOKPGE----TRLDLVEKNLKFPSLDVQVWASGFDGI 118  
OY 126 FVNTINPLDVVAALQESSGLPHRIGCMAGMLDSSRRFRMTADLEVSPPVQGMVIG 185  
DB 119 FLI-ATNPVDILTATATWKLKSGPKNRVSGSTLDTARFROSIAEMVNVDAARV 177  
OY 186 VHGDHVPPLSRATVNGIPLSEFVKK-KMIOEVDIVQKTRVAGGEIVRLIGOGSAY 244  
DB 178 EHODTELPWMSHADIGVVEELITRNPEKMDLQQLVNRDAAYHIK--KGAITY 235  
OY 245 APGASAIQMAESYLDRKRVMWCYLOGGVONHYLGPVYIGRGVEKITELELTAQ 304  
DB 236 GIAMGLARITKALINNENSVLFTVSTYLDGEGYGEKOVYIGVPAVNVRTGITREIELTSET 295  
OY 305 EROELOGSIDEVKEK 319  
DB 296 EOKRFTHSSTVLKEI 310

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